

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 19:11:10 ; Search time 38 Seconds
(without alignments)
25.320 Million cell updates/sec

Title: US-10-047-945-1

Perfect score: 54

Sequence: 1 LKAMDPTPPL 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	50.0	10	2	A36454
2	24	44.4	8	2	S21288
3	21	38.9	10	2	C35389
4	21	38.9	10	2	B39272
5	20	37.0	5	2	B60274
6	20	37.0	8	2	S10783
7	19	35.2	9	2	B30572
8	19	35.2	9	2	A60108
9	19	35.2	9	2	S26508
10	19	35.2	10	2	C30572
11	18	33.3	4	2	I51049
12	18	33.3	8	2	S17919
13	18	33.3	10	2	PC2171
14	18	33.3	10	2	A61007
15	17	31.5	10	2	A61218
16	17	31.5	10	2	B61218
17	16	29.6	5	2	B37988
18	16	29.6	9	2	D48186
19	16	29.6	9	4	S15594
20	16	29.6	10	2	PH1633
21	15	27.8	8	4	I54017
22	15	27.8	9	2	S63491
23	15	27.8	9	2	S15850
24	15	27.8	10	2	B39517
25	15	27.8	10	2	PH1592
26	15	27.8	10	2	PT0664
27	15	27.8	10	2	S18396
28	15	27.8	10	2	FX0030
29	15	27.8	10	2	F33932

30	14	25.9	7	2	S71299
31	14	25.9	7	2	PT0283
32	14	25.9	7	2	A61081
33	14	25.9	8	2	B39745
34	14	25.9	8	2	S16324
35	14	25.9	8	2	PT0559
36	14	25.9	8	2	A23967
37	14	25.9	8	2	E47393
38	14	25.9	9	2	S35538
39	14	25.9	9	2	S65433
40	14	25.9	9	2	B41983
41	14	25.9	9	2	A43065
42	14	25.9	9	2	A26744
43	14	25.9	9	2	A61057
44	14	25.9	9	2	A60579
45	14	25.9	9	2	B60246

ALIGNMENTS

RESULT 1

A36454

trypsin-modulating oostatic factor - yellow fever mosquito

C/Species: Aedes aegypti (yellow fever mosquito)

C/Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004

C/Accession: A36454; A61630

R/Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

FASEB J. 4, 3015-3020, 1990

A/Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi

A/Reference number: A36454; PMID:90367888; PMID:2394318

A/Accession: A36454

A/Molecule type: protein

A/Residues: 1-10 <BOR>

A/Cross-references: UNIPROT:P19425

R/Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

Insect Biochem. Mol. Biol. 23, 703-712, 1993

A/Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost

A/Reference number: A61630; PMID:93357794; PMID:8353526

A/Accession: A61630

A/Molecule type: protein

A/Residues: 1-10 <BO2>

A/Note: none of the amino acids is modified

C/Function:

A/Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ep

C/Keywords: hormone

Query Match 50.0%; Score 27; DB 2; Length 10;

Best Local Similarity 80.0%; Pred. No. 58;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPP 9

Db 2 DPAPP 6

RESULT 2

S21288

lectin - potato (fragment)

C/Species: Solanum tuberosum (potato)

C/Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004

C/Accession: S21288

R/Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.

Biochem. J. 283, 813-821, 1992

A/Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization

A/Reference number: S21288; PMID:92272683; PMID:1590771

A/Accession: S21288

A/Molecule type: protein

A/Residues: 1-8 <MIL>

A/Cross-references: UNIPROT:Q7M1V6

A/Experimental source: var. Ulster Sceptre.

C/Function:

A/Description: may be involved in defence mechanism of the plant

C;Keywords: hydroxyproline; lectin

Query Match 44.4%; Score 24; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTPP 9
| | | |
Db 2 ASTPSP 8

RESULT 3

C35389

urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)

C;Species: Morganella morganii

C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004

C;Accession: C35389

R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.

J. Bacteriol. 172, 3073-3080, 1990

A;Title: Morganella morganii urease: purification, characterization, and isolation of ge

A;Reference number: A35389; MUID:90264298; PMID:2345135

A;Accession: C35389

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <HUA>

A;Cross-references: UNIPROT:P17339

C;Keywords: hydrolase

Query Match 38.9%; Score 21; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPP 9
| | | |
Db 1 MQLTTP 6

RESULT 4

B59272

peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain

N;Alternate names: peptide N-glycosidase

C;Species: Prunus dulcis var. sativa (sweet almond)

C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C;Accession: B59272

R;Altman, F.; Faschinger, K.; Dalik, T.; Vorauer, K.

Eur. J. Biochem. 252, 118-123, 1998

A;Title: Characterisation of peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine amidase A

A;Reference number: A59272; MUID:98181894; PMID:9523720

A;Accession: B59272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <ALT>

A;Cross-references: UNIPROT:P81898

C;Keywords: hydrolase

Query Match 38.9%; Score 21; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 6.6e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPTP 8
| | | |
Db 1 EPTP 4

RESULT 5

B60274

major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)

C;Species: Mycobacterium tuberculosis

C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993

C;Accession: B60274

R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991

A;Title: Isolation and partial characterization of major protein antigens in the culture

A;Reference number: A60274; MUID:91099989; PMID:1898899

A;Accession: B60274

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <NAG>

Query Match 37.0%; Score 20; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTP 8
| | | |
Db 1 DPAP 4

RESULT 6

S10783

enamelin f - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998

C;Accession: S10783

R;Strawich, E.; Glimcher, M.J.

Eur. J. Biochem. 191, 47-56, 1990

A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu

A;Reference number: S10780; MUID:90336641; PMID:2379503

A;Accession: S10783

A;Molecule type: protein

A;Residues: 1-8 <STR>

C;Keywords: enamel; phosphoprotein

Query Match 37.0%; Score 20; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTPP 9
| | | |
Db 2 PLPP 5

RESULT 7

B30572

T-cell receptor beta chain C region (CRTB29) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Apr-1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997

C;Accession: B30572

R;Williams, C.B.; Gutman, G.A.

J. Immunol. 142, 1027-1035, 1989

A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utiliz

A;Reference number: A30563; MUID:89110038; PMID:2563271

A;Accession: B30572

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-9 <WIL>

C;Keywords: T-cell receptor

Query Match 35.2%; Score 19; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TPP 9
| | | |
Db 7 TPP 9

RESULT 8

A60108

exotoxin A - Streptococcus pyogenes (strain C203.S) (fragment)

N;Alternate names: blastogen A; scarlet fever toxin

C;Species: Streptococcus pyogenes

C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004

C;Accession: A60108

R;Schlievert, P.M.; Gray, E.D.

Infect. Immun. 57, 1865-1867, 1989

metallothionein-A - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)

RESULT 14

A61007
hementin (EC 3.4.-.-) - Amazon leech (fragment)
C:Species: Haementeria ghilianii (Amazon leech)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A61007
R:Swadesh, J.K.; Huang, I.Y.; Budzynski, A.Z.
J. Chromatogr. 502, 359-369, 1990
A:Title: Purification and characterization of hementin, a fibrinogenolytic protease from
A:Reference number: A61007; MUID:90256973; PMID:2187898
A:Accession: A61007
A:Molecule type: protein
A:Residues: 1-10 <SWA>
A:Cross-references: UNIPROT:Q7M3P9
C:Keywords: anticoagulant; hydrolase; saliva

Query Match 33.3%; Score 18; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 DTPPL 10
: | |
Db 5 EEPDL 10

RESULT 15

A61218
alpha-gliadin 4Ha - grass (Haynaldia villosa) (fragment)
C:Species: Haynaldia villosa, Dasypyrum villosum
C:Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C:Accession: A61218
R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.
Biochem. Genet. 29, 207-211, 1991
A:Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia
A:Reference number: A61218; MUID:91315394; PMID:1859356
A:Accession: A61218
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SHE>
A:Cross-references: UNIPROT:Q7M1F7
C:Keywords: seed; storage protein

Query Match 31.5%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 FPPPL 10
: | |
Db 5 PVPQL 9

Search completed: May 26, 2005, 19:23:37
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 19:07:01 ; Search time 166 Seconds
(without alignments)
30.848 Million cell updates/sec

Title: US-10-047-945-1
Perfect score: 54
Sequence: 1 LKAWDPPTPL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 2548

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	50.0	10	1 TMOF_AEDAE	P19425 aedes aegypti
2	24	44.4	8	2 Q7M1V6	Q7M1V6 solanum tub
3	23	42.6	10	2 Q76MK5	Q76MK5 eurypharynx
4	21	38.9	9	2 Q6SP94	Q6SP94 chlamydomon
5	21	38.9	9	2 Q39193	Q39193 pseudomonas
6	21	38.9	10	1 PNAS_PRUDU	P18988 prunus dulci
7	21	38.9	10	1 URE3_MORMO	P17339 morganella
8	21	38.9	10	2 Q67BK2	Q67BK2 klebsiella
9	20	37.0	7	1 UF04_MOUSE	P38642 mus musculus
10	20	37.0	10	2 Q91WZ3	Q91WZ3 rattus sp.
11	20	37.0	10	2 Q75595	Q75595 human immun
12	19	35.2	9	2 Q7M2W9	Q7M2W9 bos taurus
13	19	35.2	10	1 FAR5_MACRS	P83278 macrobrachi
14	19	35.2	10	1 UHA3_HUMAN	P40930 homo sapien
15	19	35.2	10	2 P90391	P90391 tomato yell
16	19	35.2	10	2 Q8JV66	Q8JV66 polyomaviru
17	19	35.2	10	2 Q8JV68	Q8JV68 polyomaviru
18	19	35.2	10	2 Q8JV70	Q8JV70 polyomaviru
19	19	35.2	10	2 Q8JV72	Q8JV72 polyomaviru
20	19	35.2	10	2 Q8JV74	Q8JV74 polyomaviru
21	19	35.2	10	2 Q8JV76	Q8JV76 polyomaviru
22	19	35.2	10	2 Q8JV80	Q8JV80 polyomaviru
23	19	35.2	10	2 Q8JV82	Q8JV82 polyomaviru
24	19	35.2	10	2 Q9Q0V7	Q9Q0V7 polyomaviru
25	19	35.2	10	2 Q9Q0V9	Q9Q0V9 polyomaviru
26	19	35.2	10	2 Q9Q0W1	Q9Q0W1 polyomaviru
27	19	35.2	10	2 Q9Q0W3	Q9Q0W3 polyomaviru
28	19	35.2	10	2 Q9Q0W5	Q9Q0W5 polyomaviru
29	19	35.2	10	2 Q9Q0W7	Q9Q0W7 polyomaviru
30	19	35.2	10	2 Q9Q0W9	Q9Q0W9 polyomaviru
31	19	35.2	10	2 Q9Q0X1	Q9Q0X1 polyomaviru

32	19	35.2	10	2	Q9Q0X3	Q9Q0X3 polyomaviru
33	19	35.2	10	2	Q9Q0X5	Q9Q0X5 polyomaviru
34	19	35.2	10	2	Q9Q0X9	Q9Q0X9 polyomaviru
35	18	33.3	8	2	Q6UA69	Q6UA69 carassius c
36	18	33.3	8	2	Q7LZ46	Q7LZ46 ctenopharyn
37	18	33.3	10	2	Q7M3P9	Q7M3P9 haementeria
38	18	33.3	10	2	Q76MM1	Q76mm1 eurypharynx
39	18	33.3	10	2	Q9S905	Q9S905 glycine max
40	18	33.3	10	2	Q8VHM9	Q8Vhm9 mus musculu
41	18	33.3	10	2	Q84140	Q84140 influenza a
42	17	31.5	8	2	Q6U7R2	Q6U7r2 cryptococcu
43	17	31.5	9	2	Q70TJ2	Q70tj2 staphylococ
44	17	31.5	10	2	Q7SA62	Q7sa62 neurospora
45	17	31.5	10	2	Q7M1P6	Q7m1f6 haynaldia v

ALIGNMENTS

RESULT 1
TMOF_AEDAE
ID TMOF_AEDAE STANDARD; PRT; 10 AA.
AC P19425;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, last sequence update)
DE 25-OCT-2004 (Rel. 45, last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like
enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
[2]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=93357794; PubMed=8353526; DOI=10.1016/0965-1748(93)90044-S;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -I- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
in the midgut which indirectly reduces the vitellogenin
concentration in the hemolymph resulting in inhibition of oocyte
development.
CC -I- DEVELOPMENTAL STAGE: Synthesized and released from follicular
epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs
and stops at 56 hrs.
DR PIR; A36454; A36454.
KW Direct protein sequencing; Hormone.
FT DOMAIN 1 10 Poly-Pro.
FT VARIANT 3 10 YD -> DY (in TMOF(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236D0A7777776DC7 CRC64;

Query Match 50.0%; Score 27; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPP 9
|||
Db 2 DPAPP 6

RESULT 2
Q7M1V6 PRELIMINARY; PRT; 8 AA.
ID Q7M1V6
AC Q7M1V6;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Lectin (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RA Millar D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R.,
 RA Bolwell G.P.;
 RT "Chitin-binding proteins in potato (Solanum tuberosum L.) tuber.
 RT Characterization, immunolocalization and effects of wounding.";
 RL Biochem. J. 283:813-821(1992).
 DR PIR; S21288; S21288.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 771 MW; C37775A771B5BDDA CRC64;

 Query Match 44.4%; Score 24; DB 2; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.6e+06;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 QY 3 AMDPTPP 9
 Db | | | |
 2 ASTFSP 8

 RESULT 3
 Q76MK5 PRELIMINARY; PRT; 10 AA.
 AC Q76MK5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ATPase subunit 8 (Fragment).
 GN NamesATPase 8;
 OS Eurypharynx pelecyanoides (pelican eel).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 OX NCBI_TaxID=55117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22967687; PubMed=12949142; DOI=10.1093/molbev/msg206;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
 RT scale gene rearrangements originated within the eels.";
 RL Mol. Biol. Evol. 20:1917-1924(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AS046487; BAB87160.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;

 Query Match 42.8%; Score 23; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 4 MDPTP 8
 Db | | | |
 4 LDPSP 8

 RESULT 4
 Q6SP94 PRELIMINARY; PRT; 9 AA.
 AC Q6SP94;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE PF26 (Fragment).
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadales; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CC-2290;
 RX MEDLINE=22570934; PubMed=12684385; DOI=10.1128/EC.2.2.362-379.2003;
 RA Kathir P., LaVoie M., Brazelton W.J., Haas N.A., Lefebvre P.A.,
 RA Silflow C.D.;
 RT "Molecular map of the Chlamydomonas reinhardtii nuclear genome.";
 RL Eukaryotic Cell 2:362-379(2003).
 DR EMBL; AY454155; AAR20844.1; -.
 FT NON_TER 1 1
 FT NON_TER 9 AA; 1012 MW; DB0AAB1B1B07776D CRC64;

 Query Match 38.9%; Score 21; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 6 PTPP 9
 Db | | | |
 1 PAPP 4

 RESULT 5
 Q99193 PRELIMINARY; PRT; 9 AA.
 AC Q99193;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE RpoB beta-subunit of RNA polymerase (Fragment).
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Borodin A.M., Danilovich A.V., Allikmets R.L., Rostapshov V.M.,
 RA Chernov I.P., Azhikina T.L., Monastyrskaya S., Sverdlov D.;
 RT "Nucleotide sequence of the rpoB gene coding for the beta-subunit of
 RT RNA polymerase in Pseudomonas putida.";
 RL Dokl. Biochem. 302:1261-1265(1988).
 DR EMBL; X15849; CAA33847.1; -.
 FT NON_TER 9 9
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 852 MW; 5B4167776DC76727 CRC64;

 Query Match 38.9%; Score 21; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 6 PTPP 9
 Db | | | |
 4 PAPP 7

 RESULT 6
 PNAS_PRUDU STANDARD; PRT; 10 AA.
 ID PNAS_PRUDU
 AC P81898;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A small
 DE chain (EC 3.5.1.52) (PNGase A subunit B) (Glycopeptide N-glycosidase)
 DE (N-glycanase) (Fragment).

OS Prunus dulcis (Almond) (Prunus amygdalus).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCBI_TaxID=3755;
 RN [1]
 RP SEQUENCE, SUBUNIT, AND MASS SPECTROMETRY.
 RX PubMed=9523720;
 RA Altmann F.; Faschinger K.; Dalik T.; Voraue K.;
 RT "Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine
 RT amidase A and its N-glycans";
 RL Eur. J. Biochem. 252:118-123(1998).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of an N(4)-(acetyl-beta-D-
 CC glucosaminyl)asparagine residue in which the N-acetyl-beta-D-
 CC glucosamine residue may be further glycosylated, to yield a
 CC (substituted) N-acetyl-beta-D-glucosaminylamine and the peptide
 CC containing an aspartic residue.
 CC -1- SUBUNIT: Heterodimer of a large and a small chain.
 CC -1- PTM: Is highly glycosylated and is resistant against self-
 CC deglycosylation.
 CC -1- MASS SPECTROMETRY: MW=21247; METHOD=MALDI; RANGE=1-10; NOTE=Ref.1.
 DR PIR; B59272; B59272.
 KW Direct protein sequencing; Glycoprotein; Hydrolase.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1149 MW; 863278CAA1E73771 CRC64;

Query Match 38.9%; Score 21; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 4.3e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DPTP 8
 :|||
 Db 1 EPTP 4

RESULT 7
 URE3_MORMO STANDARD; PRT; 10 AA.
 ID URE3_MORMO STANDARD; PRT; 10 AA.
 AC P17339;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Urease gamma subunit (EC 3.5.1.5) (Urea amidohydrolase gamma subunit)
 DE (Urease 6 kDa subunit) (Fragment).
 GN Name=ureA;
 OS Morganella morganii (Proteus morganii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Morganella.
 OX NCBI_TaxID=582;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90264298; PubMed=2345135;
 RA Hu L.-T.; Nicholson E.B.; Jones B.D.; Lynch M.J.; Mobley H.L.T.;
 RT "Morganella morganii urease: purification, characterization, and
 RT isolation of gene sequences";
 RL J. Bacteriol. 172:3073-3080(1990).
 CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
 CC -1- SUBUNIT: (Alpha, beta, gamma)(3) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the urease gamma subunit family.
 DR PIR; C35389; C35389.
 DR HAWAP; MF_00739; -; 1.
 KW Direct protein sequencing; Hydrolase.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 38.9%; Score 21; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 4.3e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MDPTPP 9
 :|||
 Db 1 MQLTTP 6

RESULT 8

Q67BK2 PRELIMINARY; PRT; 10 AA.
 ID Q67BK2
 AC Q67BK2;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Integrase (Fragment).
 GN Name=Int11;
 OS Klebsiella pneumoniae.
 OG Plasmid pKP31.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fernandez-Burriel M.; Rodriguez-Quinones F.; Alonso R.;
 RT "A sul1-type integron with a gene cassette for aac(6')-Ib, fused in 5'
 RT with a partially deleted gene-cassette DNA region of unknown origin.";
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY370764; AAR18813.1; -.
 KW Plasmid.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1026 MW; 9B8F5E376DC1ADC1 CRC64;

Query Match 38.9%; Score 21; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 4.3e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AMDPTPP 9
 :|||
 Db 4 ATAPLPP 10

RESULT 9

UF04_MOUSE STANDARD; PRT; 7 AA.
 ID UF04_MOUSE STANDARD; PRT; 7 AA.
 AC P38642;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Unknown protein from 2D-PAGE of fibroblasts (P46) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A.; Patterson R.M.; Wichter L.L.; He C.; Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins using
 RT preparative two-dimensional gel electrophoresis";
 RL Electrophoresis 15:735-745(1994).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.0, its MW is: 46 kDa.
 CC Direct protein sequencing.
 FT NON TER 7 7
 SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 37.0%; Score 20; DB 1; Length 7;
 Best Local Similarity 75.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PTPP 9
 :|||
 Db 1 PKPP 4

RESULT 10

Q91WZ3

ID Q91WZ3 PRELIMINARY; PRT; 10 AA.
AC Q91WZ3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Luteinizing hormone/chorionic gonadotropin receptor homolog (Fragment).
DE Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=96147985; PubMed=8571710;
RA Shen Q.X., Liu H.H., Chen W.Y., Bahl O.P.;
RT "Cloning and overexpression of rat ovary LH/hCG receptor cDNA in insect cells";
RL Shi Yan Sheng Wu Xue Bao 28:283-290(1995).
DR EMBL; S80660; AAB50710.1; -;
DR GO; GO:004872; F:receptor activity; IEA.
DR GO; GO:005213; F:structural constituent of chorion (sensu In. .); IEA.
KW Chorion; Receptor.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1129 MW; 09A5F22DC417760 CRC64;

Query Match 37.0%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTPP 9
| | |
DB 2 PIPP 5

RESULT 11

Q75595 PRELIMINARY; PRT; 10 AA.
AC Q75595;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
GN Name-tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U57303; AAB17863.1; -;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1182 MW; 22252E34176AB2D7 CRC64;

Query Match 37.0%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPP 9
| | |
DB 1 MEVPDP 6

RESULT 12

Q7M2M9 PRELIMINARY; PRT; 9 AA.
AC Q7M2M9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Collagen alpha 2(VI) chain (Fragment).
OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=83209648; PubMed=6852033;
RA Jander R., Rautenberg J., Glanville R.W.;
RT "Further characterization of the three polypeptide chains of bovine and human short-chain collagen (intima collagen).";
RL Eur. J. Biochem. 133:39-46(1983).
DR PIR; S26508; S26508.
DR NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 876 MW; 681467776867605B CRC64;

Query Match 35.2%; Score 19; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTPP 9
| | |
DB 4 PGPP 7

RESULT 13

FARS_MACRS STANDARD; PRT; 10 AA.
ID FARS_MACRS STANDARD; PRT; 10 AA.
AC P83278;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide FLP5 (DRTPALRLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigorngul P., Saraithongkum W., Jaidechoey S., Longyant S.,
RA Sithigorngul W.;
RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1243.4; METHOD=MALDI; RANGE=1-10;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide) family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 10 10 Phenylalanine amide.
SQ SEQUENCE 10 AA; 1244 MW; 9A1A5334072DC771 CRC64;

Query Match 35.2%; Score 19; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 9.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 DTPPPL 10
| | |
DB 1 DRTPAL 6

RESULT 14

UHA3_HUMAN STANDARD; PRT; 10 AA.
ID UHA3_HUMAN STANDARD; PRT; 10 AA.
AC P40930;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of heart (Spot 7513) (Fragment).

```

OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RL 1994.";
RL Electrophoresis 15:1459-1465(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.8, its MW is: 47.3 kDa.
KW Direct protein sequencing.
FT NON TER 10
SQ SEQUENCE 10 AA; 1049 MW; 6BBCDE41A041B76B CRC64;

Query Match 35.2%; Score 19; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 9.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AMDPT 7
DB 1 AVEPT 5

RESULT 15
P90391
ID P90391 PRELIMINARY; PRT; 10 AA.
AC P90391;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE C2 protein (Fragment).
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TYLCV-Is;
RA Wernecke M.E., Roye M.E., McLaughlin W.A., Nakhla M.K., Maxwell D.P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84397; AAB47965.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1058 MW; 25FF98B5A775A5A7 CRC64;

Query Match 35.2%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 9.5e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPP 9
DB 1 MQPSSP 6

Search completed: May 26, 2005, 19:22:05
Job time : 168 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:45:04 ; Search time 158 Seconds
(without alignments)
24.479 Million cell updates/sec

Title: US-10-047-945-1
Perfect score: 54
Sequence: 1 LKAMDPTPL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 465227

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	2	AAW53843
2	54	100.0	10	7	ABB80222
3	50	92.6	9	7	ABB80227
4	43	79.6	8	7	ABB80228
5	30	55.6	6	4	AB68473
6	30	55.6	8	5	ABB78481
7	30	55.6	10	5	ABB78478
8	28	51.9	9	2	AAW47988
9	28	51.9	9	3	AAW86825
10	28	51.9	9	3	AAW86735
11	28	51.9	9	8	ADK07609
12	28	51.9	10	2	AAW61547
13	28	51.9	10	2	AAW93336
14	28	51.9	10	2	AAW48003
15	28	51.9	10	8	ADE97778
16	27	50.0	6	2	AAW56874
17	27	50.0	6	2	AAW63465
18	27	50.0	6	2	AAW80074
19	27	50.0	6	2	AAW19715
20	27	50.0	6	2	AAW69749
21	27	50.0	6	3	AAW37945
22	27	50.0	6	4	AAW30661
23	27	50.0	6	6	ABP58325
24	27	50.0	6	7	ADC35474
25	27	50.0	6	7	ADD10251

26	27	50.0	7	2	AAW56875
27	27	50.0	7	2	AAW63466
28	27	50.0	7	2	AAW80075
29	27	50.0	7	2	AAW19716
30	27	50.0	7	2	AAW69750
31	27	50.0	7	3	AAW37946
32	27	50.0	7	4	AAW30662
33	27	50.0	7	6	ABP58326
34	27	50.0	7	7	ADC35475
35	27	50.0	7	7	ADD10252
36	27	50.0	8	2	AAW56873
37	27	50.0	8	2	AAW63467
38	27	50.0	8	2	AAW80073
39	27	50.0	8	2	AAW19717
40	27	50.0	8	2	AAW69748
41	27	50.0	8	2	AAW45995
42	27	50.0	8	3	AAW37947
43	27	50.0	8	4	AAW30663
44	27	50.0	8	6	ABP58327
45	27	50.0	8	7	ADC35476

ALIGNMENTS

RESULT 1
AAW53843
ID AAW53843 standard; peptide; 10 AA.
XX
AC AAW53843;
XX
DT 08-JUL-1998 (first entry)
XX
DE N-terminus of opossum LTNF.
XX
KW LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;
KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
KW histamine reaction treatment.
XX
OS Didelphis virginiana.
XX
PN US5744449-A.
XX
PD 28-APR-1998.
XX
PF 03-JUN-1996; 96US-00657163.
XX
PR 10-MAY-1993; 93US-00058387.
PR 22-SEP-1994; 94US-00310340.
PA (LIPP/) LIPPS B V.
PA (LIPP/) LIPPS F W.
XX
PI Lipps FW, Lipps BV;
XX
WI, 1998-271108/24.
XX
Lethal Toxin Neutralising Factor peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.
XX
Claim 7; Col 11; lipp; English.
XX
This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the

CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins

XX SQ Sequence 10 AA;
 Query Match 100.0%; Score 54; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.033; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDTPPL 10
 Db 1 LKAMDTPPL 10
 |||||

RESULT 2
 ABB80222
 ID ABB80222 standard; peptide; 10 AA.

XX AC ABB80222;
 XX DT 06-NOV-2003 (first entry)
 XX DE Synthetic LTNP, LT-10.

XX Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.

XX OS Synthetic.
 XX PN WO2003060471-A2.
 XX PD 24-JUL-2003.

XX PF 14-JAN-2003; 2003WO-US001044.
 XX PR 14-JAN-2002; 2002US-00047945.

XX PA (LIPP/) LIPPS B V.
 XX PA (LIPP/) LIPPS F W.
 XX PI Lipps BV, Lipps FW;
 XX DR WPI; 2003-636703/60.

XX Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

XX Claim 7; Page 3; 24pp; English.

XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma.
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 54; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDTPPL 10
 Db 1 LKAMDTPPL 10
 |||||

RESULT 3
 ABB80227
 ID ABB80227 standard; peptide; 9 AA.

XX AC ABB80227;
 XX DT 06-NOV-2003 (first entry)
 XX DE Synthetic LTNP, LT-9.

XX Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.

XX OS Synthetic.
 XX PN WO2003060471-A2.
 XX PD 24-JUL-2003.

XX PF 14-JAN-2003; 2003WO-US001044.
 XX PR 14-JAN-2002; 2002US-00047945.

XX PA (LIPP/) LIPPS B V.
 XX PA (LIPP/) LIPPS F W.
 XX PI Lipps BV, Lipps FW;
 XX DR WPI; 2003-636703/60.

XX Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

XX Claim 7; Page 4; 24pp; English.

XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX Sequence 9 AA;

Query Match 92.6%; Score 50; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPP 9
 |||||
 Db 1 LKAMDPTPP 9

RESULT 4
 ABB80228
 ID ABB80228 standard; peptide; 8 AA.
 XX
 AC ABB80228;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Synthetic LTNF, LT-8.
 KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.
 XX WO2003060471-A2.
 PN
 XX 24-JUL-2003.
 PD
 XX 14-JAN-2003; 2003WO-US001044.
 XX
 PF 14-JAN-2002; 2002US-00047945.
 XX
 PR (LIPP)/ LIPPS B V.
 PA (LIPP)/ LIPPS F W.
 XX
 PI Lipps BV, Lipps FW;
 XX
 DR WPI; 2003-636703/60.
 XX
 PS Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
 XX insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 XX
 PS Claim 7; Page 4; 24pp; English.
 XX
 CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IgE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 XX
 SQ Sequence 8 AA;

Query Match 79.6%; Score 43; DB 7; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPP 9
 |||||
 Db 1 LKAMDPTPP 9

RESULT 5
 AAB68473
 ID AAB68473 standard; peptide; 6 AA.
 XX
 AC AAB68473;
 XX
 DT 23-JUL-2001 (first entry)
 XX
 DE Mutated peptide derived from integrase of Ty5-6p, residues 1092-1097.
 KW Retrotransposon; polyprotein; integrase; Ty1-copia; silent chromatin;
 KW chromosomal integration; chromosomal targeting; Ty5; aging; oncogene.
 XX
 OS Synthetic.
 OS Saccharomyces paradoxus.
 XX
 PN US6228647-B1.
 XX
 PD 08-MAY-2001.
 XX
 PF 15-JAN-1999; 99US-00232446.
 XX
 PR 15-JAN-1998; 98US-0071383P.
 XX
 PA (IOWA) UNIV IOWA STATE RES FOUND INC.
 XX
 PI Voytas DF, Gai X;
 XX
 DR WPI; 2001-342676/36.
 XX
 PS Targeting integration of retrotransposon or retrovirus into silent
 XX chromatin by transforming a cell with modified integrase having a coding
 PT sequence for a peptide portion that interacts with chromatin at desired
 PT sites.
 XX
 PS Claim 13; Col 66; 41pp; English.
 XX
 CC The present sequence represents a mutated portion of an integrase. The
 CC specification describes a method for targeting integration of
 CC retrotransposon of Ty1-copia group to desired location on a chromosome.
 CC The method uses a modified integrase in a retrotransposon, where the
 CC modified integrase contains a coding sequence for a peptide portion which
 CC specifically binds to protein bound to the chromosome or to particular
 CC nucleic acid sequences on chromosome. The method is useful for targeting
 CC integration of a retrotransposon of the Ty1-copia group to a desired
 CC location on a chromosome, especially into silent chromatin. The silent
 CC chromatin targeting of Ty5 is useful for tagging genes which are affected
 CC by aging and for studying oncogenes
 XX
 SQ Sequence 6 AA;

Query Match 55.6%; Score 30; DB 4; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDPTPP 9
 :||:|
 Db 1 LDFSP 6

RESULT 6
 ABB78481
 ID ABB78481 standard; peptide; 8 AA.
 XX
 AC ABB78481;
 XX
 DT 09-JUL-2002 (first entry)

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XX DE Gum arabic glycoprotein (GAGP) peptide motif SEQ ID NO:168.
XX KW Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;
XX KW HRGP; repetitive proline-rich protein; RPRP; arabinogalactan protein;
XX KW AGP; plant gum.
XX OS Acacia senegal.
XX OS Synthetic.
XX PN WO200178503-A2.
XX PD 25-OCT-2001.
XX PF 12-APR-2001; 2001WO-US012336.
XX PR 12-APR-2000; 2000US-00547693.
XX PA (UYOH-) UNIV OHIO.
XX PI Kieliszewski MJ;
XX WPI; 2002-041307/05.
XX DR Nucleic acids and proteins useful for producing hydroxy-proline rich
XX PT glycoproteins in plants.
XX PS Claim 5; Page 121; 326pp; English.
XX CC The present invention describes synthetic genes encoding plant gums and
XX CC other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic
XX CC acids that encode them. The nucleic acids, proteins and methods from the
XX CC present invention may be used to produce HRGPs, repetitive proline-rich
XX CC proteins (RPRPs) and arabinogalactan-proteins (AGPs) in plants via
XX CC recombinant methodologies. Also described is the expression of synthetic
XX CC genes designed from repetitive peptide sequences, such as glycoproteins
XX CC (including the peptide sequences of gum arabic glycoprotein (GAGP)).
XX CC ABL51730 to ABL51849 and ABB78401 to ABB78544 represent sequences used in
XX CC the exemplification of the present invention
XX SQ Sequence 8 AA;

Query Match 55.6%; Score 30; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPL 10
DB 1 PTPPL 5

RESULT 7
ABE78478
ID ABB78478 standard; peptide; 10 AA.
XX AC ABB78478;
XX DT 09-JUL-2002 (first entry)
XX DE Gum arabic glycoprotein (GAGP) peptide motif SEQ ID NO:165.
XX KW Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;
XX KW HRGP; repetitive proline-rich protein; RPRP; arabinogalactan protein;
XX KW AGP; plant gum.
XX OS Acacia senegal.
XX OS Synthetic.
XX PN WO200178503-A2.
XX PD 25-OCT-2001.
XX PR 12-APR-2001; 2001WO-US012336.

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XX PR 12-APR-2000; 2000US-00547693.
XX PA (UYOH-) UNIV OHIO.
XX PI Kieliszewski MJ;
XX WPI; 2002-041307/05.
XX DR Nucleic acids and proteins useful for producing hydroxy-proline rich
XX PT glycoproteins in plants.
XX PS Claim 5; Page 121; 326pp; English.
XX CC The present invention describes synthetic genes encoding plant gums and
XX CC other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic
XX CC acids that encode them. The nucleic acids, proteins and methods from the
XX CC present invention may be used to produce HRGPs, repetitive proline-rich
XX CC proteins (RPRPs) and arabinogalactan-proteins (AGPs) in plants via
XX CC recombinant methodologies. Also described is the expression of synthetic
XX CC genes designed from repetitive peptide sequences, such as glycoproteins
XX CC (including the peptide sequences of gum arabic glycoprotein (GAGP)).
XX CC ABL51730 to ABL51849 and ABB78401 to ABB78544 represent sequences used in
XX CC the exemplification of the present invention
XX SQ Sequence 10 AA;

Query Match 55.6%; Score 30; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPL 10
DB 3 PTPPL 7

RESULT 8
AAV47988
ID AAY47988 standard; peptide; 9 AA.
XX AC AAY47988;
XX DT 01-DEC-1999 (first entry)
XX DE Immunogenic peptide having a human leukocyte antigen binding motif #2599.
XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX KW immune response; T cell activation; major histocompatibility complex;
XX KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX KW vaccine; immunisation.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9945954-A1.
XX PD 16-SEP-1999.
XX PF 13-MAR-1998; 98WO-US005039.
XX PR 13-MAR-1998; 98WO-US005039.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX DR New immunogenic peptides with HLA binding motif, useful in treatment and
XX PT diagnosis of cancers and viral diseases.
XX PS Claim 1; Page 131; 150pp; English.

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Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAWDTPPL 10
 Db 1 RAQDPPPEL 9

RESULT 11
 ADK07609
 ID ADK07609 standard; peptide; 9 AA.
 XX AC
 XX ADK07609;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Hepatitis C virus CTL epitope peptide #5439.
 XX
 KW pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; epitope peptide;
 KW HLA-allele; CTL.
 XX
 OS Hepatitis C virus.
 XX
 PN WO2004011650-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 24-JUL-2003; 2003WO-EP008112.
 XX
 PR 24-JUL-2002; 2002AT-00001124.
 PR 11-JUL-2003; 2003EP-00450171.
 XX
 PA (INTE-) INTERCELL AG.
 XX
 PI Mattner F, Schmidt W, Habel A;
 XX
 DR WPI; 2004-169243/16.
 XX
 PT New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.
 XX
 PS Claim 14; Page 162; 220pp; English.
 XX
 CC This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a hepatitis C virus CTL epitope peptide of the
 CC invention.
 XX
 SQ Sequence 9 AA;

Query Match 51.9%; Score 28; DB 8; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPL 10
 Db 4 PTPPM 8

RESULT 12
 AAR61547
 ID AAR61547 standard; peptide; 10 AA.
 XX AC
 XX AAR61547;
 XX
 DT 25-MAR-2003 (revised)

DT 11-MAY-1995 (first entry)
 XX
 DE Peptide fragment (1.0507) of HCV binds HLA-A2.1.
 XX
 KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV; HIV1;
 KW plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;
 KW melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;
 KW MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer;
 KW 10mer; anchor; human leukocyte antigen.
 XX
 OS Hepatitis C virus.
 XX
 PN WO9420127-A1.
 XX
 PD 15-SEP-1994.
 XX
 PF 04-MAR-1994; 94WO-US002353.
 XX
 PR 05-MAR-1993; 93US-00027146.
 PR 04-JUN-1993; 93US-00073205.
 PR 29-NOV-1993; 93US-00159184.
 XX
 PA (CYTE-) CYTEL CORP.
 XX
 PI Grey HM, Sette A, Sidney J, Kast W;
 XX
 DR WPI; 1994-302678/37.
 XX
 PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for
 PT treatment or prophylaxis of cancer, virus infection or autoimmune
 PT diseases.
 XX
 PS Example 5; Page 109; 138pp; English.
 XX
 CC AAR59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1
 CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
 CC of at least 1% as compared to a reference peptide (AAR71293). AAR61547
 CC has an IC50 of 0.0042 and the sequence occurs at position 2803 in the HCV
 CC LOF protein. The peptides of the invention can induce cytotoxic T
 CC lymphocytes which can react with target cells. They can be used for the
 CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma, etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 10 AA;

Query Match 51.9%; Score 28; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 5.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPL 10
 Db 5 DPTPL 10

RESULT 13
 AAR93336
 ID AAR93336 standard; peptide; 10 AA.
 XX AC
 XX AAR93336;
 XX
 DT 24-APR-1996 (first entry)
 XX
 DE YES protein tyrosine kinase derived peptide #9.
 XX
 KW SH3 ligand; SH3 binding agent; biased phage library;
 KW recognition sequence; src SH3 domain; Paget's disease; restenosis;
 KW rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47;
 KW p67; complex; chronic myelogenous leukaemia; cancer.
 XX
 OS Synthetic.
 XX

PN WO9524419-A1.
 XX 14-SEP-1995.
 XX 13-MAR-1995; 95WO-US003208.
 XX 11-MAR-1994; 94US-00209835.
 PR 06-JAN-1995; 95US-00369832.
 XX (ARIA-) ARIAD PHARM INC.
 XX Rickles RJ, Brugge JS, Botfield MC, Zoller MJ;
 XX WPI; 1995-328231/42.
 XX Identification of peptide(s) binding specifically to SH3 domains - for
 PT use in inhibiting interactions mediated by SH3 domains in treatment of
 PT e.g. osteoporosis and cancer.
 XX Disclosure; Fig 1; 74pp; English.
 XX The sequences given in AAR93272-342 represent peptides which are SH3
 CC ligands/SH3 binding agents. They represent a biased phage library which
 CC comprises six random amino acids flanking the tetrapeptide -PPIP which
 CC was identified as a recognition sequence for the src SH3 domain. These
 CC sequences were identified using the method of the invention. The method
 CC comprises contacting the SH3 domain with a mixture of peptides under
 CC conditions permitting a ligand to bind to an SH3 domain to form a
 CC complex. Any unbound peptides are removed and the complexed peptide
 CC ligands are dissociated from the complexes. The selected peptides are
 CC enriched by re-contacting them with the SH3 domain and then candidates
 CC which bind to the SH3 domain are detected. The isolated SH3 binding
 CC peptides may be used in the diagnosis, prevention and treatment of
 CC conditions or diseases resulting from cellular processes mediated by an
 CC SH3-based interaction. Such diseases include Paget's disease. Other
 CC conditions treatable with these peptides include restenosis, rheumatoid
 CC arthritis, gout and other problems in which an SH3 of neutrophil oxidase
 CC p47 and p67 complex is implicated, etc
 XX Sequence 10 AA;
 SQ Query Match 51.9%; Score 28; DB 2; Length 10;
 Best Local Similarity 55.6%; Pred. No. 5.6e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 KAMDPTPL 10
 Db ||| |||
 1 KAKRPLPI 9
 RESULT 14
 AAY48003
 ID AAY48003 standard; peptide; 10 AA.
 XX AAY48003;
 AC
 XX 01-DEC-1999 (first entry)
 DT
 DE Immunogenic peptide having a human leukocyte antigen binding motif #2614.
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9945954-A1.
 PN 16-SEP-1999.
 XX

PF 13-MAR-1998; 98WO-US005039.
 XX 13-MAR-1998; 98WO-US005039.
 XX (EPIM-) EPIMUNE INC.
 XX Sette A, Kubo RT, Sidney J, Cellis E, Grey HM, Southwood S;
 PI WPI; 1999-551214/46.
 XX New immunogenic peptides with HLA binding motif, useful in treatment and
 PT diagnosis of cancers and viral diseases.
 XX Claim 1; Page 132; 150pp; English.
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above
 XX Sequence 10 AA;
 SQ Query Match 51.9%; Score 28; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 5.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 DPTPL 10
 Db ||| |||
 1 DPTPL 6
 RESULT 15
 ADE97778
 ID ADE97778 standard; peptide; 10 AA.
 XX ADE97778;
 AC
 XX 12-FEB-2004 (first entry)
 DT
 DE Immunogenic HLA-A2.1 binding peptide #260.
 XX Cytostatic; anti-inflammatory; hepatotropic; virucide; anti-HIV;
 KW nephrotropic; neuroprotective; antiarthritic; antirheumatic;
 KW immunosuppressive; dermatological; muscular; nephrotropic; thyromimetic;
 KW haemostatic; antithyroid; antianaemic; anabolic; hypertensive;
 KW immunogenic peptide composition; immune response; prostate cancer;
 KW hepatitis B; hepatitis C; AIDS; renal carcinoma; cervical carcinoma;
 KW lymphoma; cytomegalovirus; CMV; condyloma acuminatum;
 KW autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis;
 KW Sjogren syndrome; scleroderma; polymyositis; dermatomyositis;
 KW systemic lupus erythematosus; juvenile rheumatoid arthritis;
 KW ankylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid;
 KW pemphigus; glomerulonephritis; Goodpasture's syndrome;
 KW autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;
 KW idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease;
 KW human leukocyte antigen A2.1; HLA A2.1;
 KW immunogenic HLA-A2.1 binding peptide.

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XX Synthetic.
XX OS
XX PN US2003185822-A1.
XX PD
XX PF 02-OCT-2003.
XX PR
XX PR 03-APR-2002; 2002US-00116557.
XX PR 05-MAR-1993; 93US-00027146.
XX PR 04-JUN-1993; 93US-00073205.
XX PR 29-NOV-1993; 93US-00159184.
XX PR 02-DEC-1994; 94US-00349177.
XX PA (GREY/) GREY H M.
XX PA (SETT/) SETTE A.
XX PA (SIDN/) SIDNEY J.
XX PI Grey HM, Sette A, Sidney J;
XX PI WPI; 2004-041186/04.
XX DR
XX PT Immunogenic peptide composition for preventing, treating or diagnosing
XX PT pathological states, e.g. prostate cancer, hepatitis B and C, Acquired
XX PT Immunodeficiency Syndrome, and renal carcinoma, includes conserved
XX PT residues at specified positions.
XX PS Example 11; Page 25; 38pp; English.
XX CC The invention describes an immunogenic peptide composition comprising 9
XX CC residues including a first conserved residue at a second position from N-
XX CC terminus, and a second conserved residue at C-terminal position. The
XX CC inventive peptide composition is used to elicit an immune response
XX CC against a desired antigen for preventing, treating or diagnosing
XX CC pathological states, e.g. prostate cancer, hepatitis B, hepatitis C,
XX CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, cytomegalovirus
XX CC (CMV), and condyloma acuminatum. It is also used to treat autoimmune
XX CC associated disorders, e.g. multiple sclerosis, rheumatoid arthritis,
XX CC Sjogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic
XX CC lupus erythematosus, juvenile rheumatoid arthritis, ankylosing
XX CC spondylitis, myasthenia gravis (MG), bullous pemphigoid, pemphigus,
XX CC glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia,
XX CC Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic
XX CC purpura, Grave's disease, and Addison's disease. The invention defines
XX CC positions within a motif enabling the selection of the peptides which
XX CC will bind efficiently to human leukocyte antigen (HLA) A2.1. This is the
XX CC amino acid sequence of an immunogenic HLA-A2.1 binding peptide.
XX SQ Sequence 10 AA;
Query Match 51.9%; Score 28; DB 8; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 DPTPL 10
DB 5 DPTPL 10
Search completed: May 26, 2005, 19:19:14
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-10-047-945-1

Perfect score: 54

Sequence: 1 LKAMDPTPL 10

Scoring table: BLOSUM62

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Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 185832

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Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	14	US-10-047-945-1
2	50	92.6	9	14	US-10-047-945-6
3	43	79.6	8	14	US-10-047-945-7
4	30	55.6	8	15	US-10-437-708-168
5	30	55.6	8	17	US-10-418-032-168
6	30	55.6	10	15	US-10-437-708-165
7	30	55.6	10	17	US-10-418-032-165
8	28	51.9	9	8	US-08-344-824-273
9	28	51.9	10	8	US-08-344-824-381
10	27	50.0	8	9	US-09-758-128-20
11	27	50.0	8	9	US-09-758-128-23
12	27	50.0	8	9	US-09-758-128-26
13	27	50.0	8	9	US-09-758-128-29

14	27	50.0	8	9	US-09-758-426-20	Sequence 20, Appl
15	27	50.0	8	9	US-09-758-426-23	Sequence 23, Appl
16	27	50.0	8	9	US-09-758-426-26	Sequence 26, Appl
17	27	50.0	8	9	US-09-758-426-29	Sequence 29, Appl
18	27	50.0	8	9	US-09-758-198-20	Sequence 20, Appl
19	27	50.0	8	9	US-09-758-198-23	Sequence 23, Appl
20	27	50.0	8	9	US-09-758-198-26	Sequence 26, Appl
21	27	50.0	8	9	US-09-758-198-29	Sequence 29, Appl
22	27	50.0	8	10	US-09-861-661-20	Sequence 20, Appl
23	27	50.0	8	10	US-09-861-661-23	Sequence 23, Appl
24	27	50.0	8	10	US-09-861-661-26	Sequence 26, Appl
25	27	50.0	8	10	US-09-861-661-29	Sequence 29, Appl
26	27	50.0	9	10	US-09-935-430-7	Sequence 7, Appl
27	27	50.0	9	14	US-10-224-999A-1613	Sequence 1613, Ap
28	27	50.0	9	14	US-10-277-292-7	Sequence 7, Appl
29	27	50.0	9	15	US-10-280-340-7	Sequence 7, Appl
30	27	50.0	9	15	US-10-149-138-2002	Sequence 2002, Ap
31	27	50.0	9	15	US-10-149-138-4046	Sequence 4046, Ap
32	27	50.0	9	15	US-10-149-138-4159	Sequence 4159, Ap
33	27	50.0	9	15	US-10-398-104-47	Sequence 47, Appl
34	27	50.0	9	16	US-10-149-138-2002	Sequence 2002, Ap
35	27	50.0	9	16	US-10-149-138-4046	Sequence 4046, Ap
36	27	50.0	9	16	US-10-149-138-4159	Sequence 4159, Ap
37	27	50.0	9	17	US-10-330-300-52	Sequence 52, Appl
38	27	50.0	10	10	US-09-935-430-74	Sequence 74, Appl
39	27	50.0	10	10	US-09-935-430-619	Sequence 619, App
40	27	50.0	10	14	US-10-224-999A-1619	Sequence 1619, App
41	27	50.0	10	14	US-10-224-999A-1620	Sequence 1620, Ap
42	27	50.0	10	14	US-10-277-292-74	Sequence 74, Appl
43	27	50.0	10	14	US-10-277-292-619	Sequence 619, App
44	27	50.0	10	15	US-10-280-340-74	Sequence 74, Appl
45	27	50.0	10	15	US-10-280-340-619	Sequence 619, App

ALIGNMENTS

RESULT 1
US-10-047-945-1
; Sequence 1, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED.
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-1

Query Match 100.0%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPL 10
Db 1 LKAMDPTPL 10

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RESULT 2
US-10-047-945-6
; Sequence 6, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.
US-10-047-945-6
Query Match          92.6%; Score 50; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDTPP 9
   |||||
Db 1 LKAMDTPP 9

RESULT 3
US-10-047-945-7
; Sequence 7, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
US-10-047-945-7
Query Match          79.6%; Score 43; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDTPP 8
   |||||
Db 1 LKAMDTPP 8

RESULT 4
US-10-437-708-168
; Sequence 168, Application US/10437708
; Publication No. US20040009555A1
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/10/437,708
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US/09/547,693
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 168
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; NAME/KEY: SITE
; LOCATION: (3)..(4)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-437-708-168
Query Match          55.6%; Score 30; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPL 10
   |||||
Db 1 PTPPL 5

RESULT 5
US-10-418-032-168
; Sequence 168, Application US/10418032
; Publication No. US20050074838A1
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; FILE REFERENCE: OHU-07775
; CURRENT APPLICATION NUMBER: US/10/418,032
; CURRENT FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 168
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(4)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-418-032-168
Query Match          55.6%; Score 30; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPL 10
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Db          1 PTPPL 5

RESULT 6
US-10-437-708-165
; Sequence 165, Application US/10437708
; Publication No. US20040009555A1
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; TITLE OF INVENTION: Glycoproteins
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/10/437,708
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US/09/547,693
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 165
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)..(3)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)..(6)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-437-708-165
Query Match          55.6%; Score 30; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy          6 PTPPL 10
          |||||
Db          3 PTPPL 7

RESULT 7
US-10-418-032-165
; Sequence 165, Application US/10418032
; Publication No. US20050074838A1
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; TITLE OF INVENTION: Glycoproteins
; FILE REFERENCE: OHU-07775
; CURRENT APPLICATION NUMBER: US/10/418,032
; CURRENT FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 165
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: MISC FEATURE
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; LOCATION: (3)..(3)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (5)..(6)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-418-032-165
Query Match          55.6%; Score 30; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy          6 PTPPL 10
          |||||
Db          3 PTPPL 7

RESULT 8
US-08-344-824-273
; Sequence 273, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 273:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-344-824-273

Query Match          51.9%; Score 28; DB 8; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy          5 DPTPPL 10
          |||||
Db          1 DPTPPL 6

RESULT 9
US-08-344-824-381
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; Sequence 381, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 381:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-381

Query Match 51.9%; Score 28; DB 8; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPPL 10
|:|:|
Db 1 DPTPPL 6

RESULT 10
US-09-758-128-20
; Sequence 20, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mouse
US-09-758-128-26

; TYPE: PRT
; ORGANISM: Bovine
US-09-758-128-20

Query Match 50.0%; Score 27; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AMDPTPPL 10
|:|:|
Db 1 AISPTPAL 8

RESULT 11
US-09-758-128-23
; Sequence 23, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Porcine
US-09-758-128-23

Query Match 50.0%; Score 27; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AMDPTPPL 10
|:|:|
Db 1 AISPTPAL 8

RESULT 12
US-09-758-128-26
; Sequence 26, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mouse
US-09-758-128-26

Query Match 50.0%; Score 27; DB 9; Length 8;

Best Local Similarity 62.5%; Pred. No. 1.3e+06; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 1;

Qy 3 AMDPTPPL 10
|: ||| |
Db 1 AISPTPAL 8

RESULT 13

US-09-758-128-29
; Sequence 29, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758.128
; CURRENT FILING DATE: 2001-01-12
; PRIOR FILING DATE: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rat
US-09-758-128-29

Query Match 50.0%; Score 27; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AMDPTPPL 10
|: ||| |
Db 1 AISPTPAL 8

RESULT 14

US-09-758-426-20
; Sequence 20, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020169116A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758.426
; CURRENT FILING DATE: 2001-01-12
; PRIOR FILING DATE: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Bovine
US-09-758-426-20

Query Match 50.0%; Score 27; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AMDPTPPL 10
|: ||| |

Db

1

AISPTPAL 8

RESULT 15

US-09-758-426-23
; Sequence 23, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020169116A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758.426
; CURRENT FILING DATE: 2001-01-12
; PRIOR FILING DATE: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Porcine
US-09-758-426-23

Query Match 50.0%; Score 27; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AMDPTPPL 10
|: ||| |
Db 1 AISPTPAL 8

Search completed: May 26, 2005, 19:35:47
Job time : 188 secs

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OM protein - protein search, using sw model

Run on: May 26, 2005, 19:08:54 ; Search time 41 Seconds
(without alignments)
18.207 Million cell updates/sec

Title: US-10-047-945-1

Perfect score: 54

Sequence: 1 LKMDPTPPL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 115750

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	10	1	US-08-657-163A-2
2	30	55.6	8	3	US-09-232-446B-24
3	30	55.6	8	4	US-09-547-693-168
4	30	55.6	10	4	US-09-547-693-165
5	27	50.0	6	1	US-07-989-290-2
6	27	50.0	6	1	US-08-271-698-2
7	27	50.0	6	1	US-08-468-596-2
8	27	50.0	6	4	US-08-295-996B-12
9	27	50.0	6	4	US-09-295-846B-15
10	27	50.0	6	4	US-09-551-737C-15
11	27	50.0	6	4	US-09-295-924B-2
12	27	50.0	6	4	US-09-551-738B-12
13	27	50.0	7	1	US-07-989-290-3
14	27	50.0	7	1	US-08-271-698-3
15	27	50.0	7	1	US-08-468-596-3
16	27	50.0	7	4	US-09-295-996B-13
17	27	50.0	7	4	US-09-295-846B-16
18	27	50.0	7	4	US-09-551-737C-16
19	27	50.0	7	4	US-08-295-924B-3
20	27	50.0	7	4	US-09-551-738B-13
21	27	50.0	8	1	US-07-989-290-4
22	27	50.0	8	1	US-08-271-698-4
23	27	50.0	8	1	US-08-468-596-4
24	27	50.0	8	4	US-09-295-996B-14
25	27	50.0	8	4	US-09-295-846B-17
26	27	50.0	8	4	US-09-551-737C-17
27	27	50.0	8	4	US-09-295-924B-4

Sequence 14, Appl
Sequence 8, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 7, Appl
Sequence 8, Appl
Sequence 40, Appl
Sequence 33, Appl
Sequence 103, Appl
Sequence 14, Appl
Sequence 9, Appl
Sequence 22, Appl
Sequence 86, Appl
Sequence 51, Appl
Sequence 12, Appl
Sequence 31, Appl
Sequence 20, Appl
Sequence 49, Appl

28 27 50.0 8 4 US-09-551-738B-14
29 27 50.0 10 4 US-09-295-996B-8
30 27 50.0 10 4 US-09-295-846B-11
31 27 50.0 10 4 US-09-551-737C-11
32 27 50.0 10 4 US-09-295-924B-7
33 27 50.0 10 4 US-09-551-738B-8
34 26 48.1 4 3 US-08-895-590-40
35 26 48.1 6 3 US-08-441-943-33
36 26 48.1 6 4 US-08-897-556A-103
37 26 48.1 7 4 US-09-641-803-14
38 26 48.1 7 4 US-09-822-270-9
39 26 48.1 9 2 US-08-416-870C-22
40 26 48.1 9 2 US-08-340-283-86
41 26 48.1 9 3 US-08-895-590-51
42 26 48.1 10 1 US-08-230-047-12
43 26 48.1 10 3 US-08-476-509B-31
44 25 46.3 9 1 US-07-972-032-20
45 25 46.3 9 1 US-07-972-032-49

RESULT 1
US-08-657-163A-2
; Sequence 2, Application US/08657163A
; Patent No. 5744449
; GENERAL INFORMATION:
; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
; TITLE OF INVENTION: SYNTHETIC LTNFS AND THEIR
; TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BINIE V. LIPPS
; STREET: 4509 MIMOSA DR.
; CITY: BELLAIRE
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
; SOFTWARE: MS WORD 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,163A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,340
; FILING DATE: 22 SEPTEMBER 1994
; CLASSIFICATION: 514
; APPLICATION NUMBER: 08/058,387
; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN R. CASPERSON
; REGISTRATION NUMBER: 28,198
; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-482-2961
; TELEFAX: 713-663-7290
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N

ALIGNMENTS

ORIGINAL SOURCE: SYNTHETIC
US-08-657-163A-2

Query Match 100.0%; Score 54; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
Db 1 LKAMDPTPPL 10

RESULT 2
US-09-232-446B-24
; Sequence 24, Application US/09232446B
; Patent No. 6228647

GENERAL INFORMATION:
; APPLICANT: Voytas, Daniel F.
; TITLE OF INVENTION: Transposable Element Protein that Directs DNA
; FILE REFERENCE: Integration to Specific Chromosomal Sites
; CURRENT APPLICATION NUMBER: US/09/232,446B
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 60/071,383
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mutant peptide
US-09-232-446B-24

Query Match 55.6%; Score 30; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPTPP 9
Db 1 LDPSPP 6

RESULT 3
US-09-547-693-168
; Sequence 168, Application US/09547693
; Patent No. 6639050

GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; FILE REFERENCE: Glycoproteins
; CURRENT APPLICATION NUMBER: US/09/547,693
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 168
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; NAME/KEY: SITE
; LOCATION: (3)..(4)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-09-547-693-168

Query Match 55.6%; Score 30; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPL 10
Db 1 PTPPL 5

RESULT 4
US-09-547-693-165
; Sequence 165, Application US/09547693
; Patent No. 6639050
GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; FILE REFERENCE: Glycoproteins
; CURRENT APPLICATION NUMBER: US/09/547,693
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 165
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; NAME/KEY: SITE
; LOCATION: (3)..(3)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; NAME/KEY: SITE
; LOCATION: (5)..(6)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-09-547-693-165

Query Match 55.6%; Score 30; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPL 10
Db 3 PTPPL 7

RESULT 5
US-07-989-290-2
; Sequence 2, Application US/07989290
; Patent No. 5358934

GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Carlson, David A.
; TITLE OF INVENTION: Materials and Methods for Control
; TITLE OF INVENTION: of Pests
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/989,290
FILING DATE: 19921211
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S&S-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-989-290-2

Query Match 50.0%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPP 9
|||
Db 2 DPAPP 6

RESULT 6

US-08-271-698-2
Sequence 2, Application US/08271698
Patent No. 5439821

GENERAL INFORMATION:
APPLICANT: Borovsky, Dov
APPLICANT: Carlson, David A.
TITLE OF INVENTION: Materials and Methods for Control
TITLE OF INVENTION: of Pests
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,698
FILING DATE: 07-JUL-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S&S-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-271-698-2

Query Match 50.0%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPP 9
|||
Db 2 DPAPP 6

RESULT 7

US-08-468-596-2
Sequence 2, Application US/08468596
Patent No. 5629196

GENERAL INFORMATION:
APPLICANT: Borovsky, Dov
APPLICANT: Carlson, David A.
TITLE OF INVENTION: Materials and Methods for Control
TITLE OF INVENTION: of Pests
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,596
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,698
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US/07/989,290
FILING DATE: 11-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S&S-127

TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-468-596-2

Query Match 50.0%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPP 9
|||
Db 2 DPAPP 6

RESULT 8

US-09-295-996B-12

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; Sequence 12, Application US/09295996B
; Patent No. 6413530
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UF-230
; CURRENT APPLICATION NUMBER: US/09/295,996B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-295-996B-12
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Query Match 50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 5 DTPPP 9
DB 2 DPAPP 6
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RESULT 9
US-09-295-846B-15
; Sequence 15, Application US/092959846B
; Patent No. 6562590
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UF-223
; CURRENT APPLICATION NUMBER: US/09/295,846B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF peptide
US-09-295-846B-15
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Query Match 50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 5 DTPPP 9
DB 2 DPAPP 6
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RESULT 10
US-09-551-737C-15
; Sequence 15, Application US/09551737C
; Patent No. 6566129
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Schlesinger, Yaagov
; APPLICANT: Nauwelaers, Sabine M. I.
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UF-223C1
; CURRENT APPLICATION NUMBER: US/09/551,737C
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/295,846
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
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; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-551-737C-15
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```
Query Match 50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 5 DTPPP 9
DB 2 DPAPP 6
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RESULT 11
US-09-295-924B-2
; Sequence 2, Application US/09295924B
; Patent No. 6593299
; GENERAL INFORMATION:
; APPLICANT: John, Bennett
; APPLICANT: Alan, Brandt
; APPLICANT: Dov, Borovski
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROLLING PESTS
; FILE REFERENCE: 4137-120
; CURRENT APPLICATION NUMBER: US/09/295,924B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ().()
; OTHER INFORMATION: Truncated TMOF
US-09-295-924B-2
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Query Match 50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 5 DTPPP 9
DB 2 DPAPP 6
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RESULT 12
US-09-551-738B-12
; Sequence 12, Application US/09551738B
; Patent No. 6635265
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Materials and Methods Useful for the Control of Insect Larvae
; FILE REFERENCE: UF-224C1
; CURRENT APPLICATION NUMBER: US/09/551,738B
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/296,113
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-551-738B-12
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Query Match 50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
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Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTTP 9
|||
Db 2 DPAPP 6

RESULT 13

US-07-989-290-3
; Sequence 3, Application US/07989290
; Patent No. 5358934

; GENERAL INFORMATION:

; APPLICANT: Borovsky, Dov

; APPLICANT: Carlson, David A.

; TITLE OF INVENTION: Materials and Methods for Control

; TITLE OF INVENTION: of Pests

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David R. Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/989,290

; FILING DATE: 19921211

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Saliwanchik, David R.

; REGISTRATION NUMBER: 31,794

; REFERENCE/DOCKET NUMBER: UF/S&S-127

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 904-375-8100

; TELEFAX: 904-372-5800

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; US-07-989-290-3

Query Match 50.0%; Score 27; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTTP 9
|||
Db 2 DPAPP 6

RESULT 14

US-08-271-698-3

; Sequence 3, Application US/08271698

; Patent No. 5439821

; GENERAL INFORMATION:

; APPLICANT: Borovsky, Dov

; APPLICANT: Carlson, David A.

; TITLE OF INVENTION: Materials and Methods for Control

; TITLE OF INVENTION: of Pests

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David R. Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,596

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/271,698

; FILING DATE: 07-JUL-1994

; APPLICATION NUMBER: US/07/989,290

; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,698
; FILING DATE: 07-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,290
; FILING DATE: 11-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF/S&S-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-271-698-3

Query Match 50.0%; Score 27; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTTP 9
|||
Db 2 DPAPP 6

RESULT 15

US-08-468-596-3

; Sequence 3, Application US/08468596

; Patent No. 5629196

; GENERAL INFORMATION:

; APPLICANT: Borovsky, Dov

; APPLICANT: Carlson, David A.

; TITLE OF INVENTION: Materials and Methods for Control

; TITLE OF INVENTION: of Pests

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David R. Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,596

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/271,698

; FILING DATE: 07-JUL-1994

; APPLICATION NUMBER: US/07/989,290

;; FILING DATE: 11-DEC-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Saliwanchik, David R.
;; REGISTRATION NUMBER: 31,794
;; REFERENCE/DOCKET NUMBER: UF/S&S-127
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 904-375-8100
;; TELEFAX: 904-372-5800
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-468-596-3

Query Match 50.0%; Score 27; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTTP 9
|||
Db 2 DPAPP 6

Search completed: May 26, 2005, 19:22:51
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 19:31:54 ; Search time 38 Seconds
(without alignments)
37.980 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKAMDPTPLWKITE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	32.1	7	2 A61081	tryptophyllin, bas
2	27	32.1	10	2 A36454	trypsin-modulating
3	27	32.1	15	2 A47628	EC gamma receptor
4	25	29.8	13	2 PH1620	Ig H chain V-D-J r
5	25	29.8	15	2 PD0444	coupling factor 6
6	24	28.6	8	2 S21288	lectin - potato (f
7	23	27.4	7	4 A58725	virotaxin - destro
8	23	27.4	12	2 I58273	thyroglobulin - ra
9	23	27.4	15	2 B61457	hypothetical 1.5K
10	23	27.4	15	2 G37286	alpha-glucosidase
11	22	26.2	13	2 D37267	Ig heavy chain C r
12	22	26.2	13	2 D37267	Ig heavy chain C r
13	22	26.2	14	2 PT0036	calotropin D1 - mu
14	22	26.2	15	2 PT0037	light harvesting c
15	21	25.0	10	2 C35389	urease (EC 3.5.1.5
16	21	25.0	10	2 B59272	peptide-N4-(N-acet
17	21	25.0	10	2 S39030	lysyl-bradykinin -
18	21	25.0	11	1 XAVIBH	bradykinin-potenti
19	21	25.0	11	2 C59151	protein-tyrosine k
20	21	25.0	15	2 PA0055	protein QF200007 -
21	21	25.0	15	2 A26212	carboxypeptidase B
22	20	23.8	5	2 B60274	major protein anti
23	20	23.8	8	2 S10783	enamelin f - bovin
24	20	23.8	8	2 A39308	glycine reductase
25	20	23.8	9	2 S78426	52.5K protein - sp
26	20	23.8	12	1 JTJGO	tremorogen A-10 -
27	20	23.8	12	2 PN0663	dystrophin-associa
28	20	23.8	14	2 PH1348	Ig heavy chain DJ
29	20	23.8	14	2 A60158	disaggregatase - M

30	20	23.8	14	2 S33801	chaperone, TCP1-re
31	20	23.8	14	2 S33802	chaperone, TCP1-re
32	20	23.8	15	2 S10891	ubiquitin thiolest
33	20	23.8	15	2 PT0093	ubiquitin thiolest
34	19	22.6	9	2 B30572	t-cell receptor be
35	19	22.6	9	2 A60108	exotoxin A - Strept
36	19	22.6	9	2 S26508	collagen alpha 2(V
37	19	22.6	10	2 C30572	T-cell receptor be
38	19	22.6	11	2 D45900	complement C3b rec
39	19	22.6	11	2 A49037	TCR gamma V-J regi
40	19	22.6	13	2 A40207	cell surface glyco
41	19	22.6	14	2 F33160	H+-transporting tw
42	19	22.6	14	2 S12904	protein kinase (EC
43	19	22.6	14	2 B56884	Pax-QNR, long form
44	19	22.6	15	2 A60929	dichloromethane de
45	19	22.6	15	2 S67918	serine proteinase

ALIGNMENTS

RESULT 1

A61081

tryptophyllin, basic - Rohde's leaf frog

C;Species: Phyllomedusa rohdei (Rohde's leaf frog)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000

C;Accession: A61081

R;Montecucchi, P.C.; Vincenti, M.; Lazarini, A.M.; Rusconi, L.; Erspamer, V.

A;Title: Isolation, structure determination and synthesis of a novel tryptophan-containi

A;Reference number: A61081

A;Accession: A61081

A;Molecule type: protein

A;Residues: 1-7 <MON>

C;Comment: The biological activity of this peptide was not determined.

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; hydroxyproline; skin

F;3/Modified site: 4-hydroxyproline (Pro) #status experimental

F;7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 32.1%; Score 27; DB 2; Length 7;

Best Local Similarity 80.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PPLWI 12

Db 2 PPSWI 6

RESULT 2

A36454

trypsin-modulating oostatic factor - yellow fever mosquito

C;Species: Aedes aegypti (yellow fever mosquito)

C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004

C;Accession: A36454; A61630

R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

FASEB J. 4, 3015-3020, 1990

A;Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi.

A;Reference number: A36454; MUID:90367888; PMID:2394318

A;Accession: A36454

A;Molecule type: protein

A;Residues: 1-10 <BOR>

A;Cross-references: UNIPROT:P19425

R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

Insect Biochem. Mol. Biol. 23, 703-712, 1993

A;Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost

A;Reference number: A61630; MUID:93357794; PMID:8353526

A;Accession: A61630

A;Molecule type: protein

A;Residues: 1-10 <BO2>

A;Note: none of the amino acids is modified

C;Function:

A;Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ep

C;Keywords: hormone

Query Match 32.1%; Score 27; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9
|||
Db 2 DPAPP 6

RESULT 3

A47628

Pc gamma receptor II (CD32) - human (fragments)

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C;Accession: A47628

R;Waxmerdam, P.A.M.; van de Winkel, J.G.J.; Gosselin, E.J.; Capel, P.J.A.

J. Exp. Med. 172, 19-25, 1990

A;Title: Molecular basis for a polymorphism of human Fc gamma receptor II (CD32).

A;Reference number: A47628; MUID:90293679; PMID:2141627

A;Accession: A47628

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-15 <WAR>

C;Keywords: immunoglobulin receptor

Query Match 32.1%; Score 27; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 MDPTPLW 11
|||
Db 1 MTAAPFCW 8

RESULT 4

PH1620

Ig H chain V-D-J-region (clone B-less 40) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1620

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1620

A;Molecule type: DNA

A;Residues: 1-13 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 29.8%; Score 25; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TPPLW 11
|||
Db 8 TPMLW 12

RESULT 5

PD0444

coupling factor 6 mitochondrial - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999

C;Accession: PD0444

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kano, M.; Morimasa, T.; Tsugita, A.

submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Contents: Striatum

A;Accession: PD0444

A;Molecule type: protein
A;Residues: 1-15 <KAW>
C;Keywords: mitochondrion

Query Match 29.8%; Score 25; DB 2; Length 15;
Best Local Similarity 36.4%; Pred. No. 5.8e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 KAMDPTPLWI 12
|||
Db 2 KELDPVQKLFV 12

RESULT 6

S21288

lectin - potato (fragment)

C;Species: Solanum tuberosum (potato)

C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004

C;Accession: S21288

R;Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.

Biochem. J. 283, 813-821, 1992

A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization

A;Reference number: S21288; MUID:92272683; PMID:1590771

A;Accession: S21288

A;Molecule type: protein

A;Residues: 1-8 <MIL>

A;Cross-references: UNIPROT:Q7MIV6

A;Experimental source: var. Ulster Sceptre

C;Function:

A;Description: may be involved in defence mechanism of the plant

C;Keywords: hydroxyproline; lectin

Query Match 28.6%; Score 24; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AWDPTTP 9
|||
Db 2 ASTPSPP 8

RESULT 7

A58725

virotaxin - destroying angel

C;Species: Amanita virosa (destroying angel)

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C;Accession: A58725

R;Paulstich, H.; Buku, A.; Bodenmueller, H.; Wieland, T.

Biochemistry 19, 334-343, 1980

A;Title: Virotaxins: actin-binding cyclic peptides of Amanita virosa mushrooms.

A;Reference number: A58725; MUID:6893271; PMID:6893271

A;Accession: A58725

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <FAU>

C;Keywords: D-amino acid; hydroxyproline; toxin; unencoded polypeptide

P;1-7/Cross-link: cyclopeptide (Val-Leu) #status experimental

F;2/Modified site: D-threonine (Thr) #status experimental

F;3/Modified site: D-serine (Ser) #status experimental

F;4/Modified site: (3R,4S)-3,4-dihydroxyproline (Pro) #status experimental

F;6/Modified site: 2'-methylsulfonyltryptophan (Trp) #status experimental

F;7/Modified site: 4,5-dihydroxyisoleucine (Leu) #status experimental

Query Match 27.4%; Score 23; DB 4; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 TPPLWI 12
|||
Db 2 TSPAWL 7

RESULT 8

I58273
thyroglobulin - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I58273
R;Musti, A.M.; Ursini, V.M.; Avvedimento, E.V.; Zimarino, V.; Di Lauro, R.
Nucleic Acids Res. 15, 8149-8166, 1987
A;Title: A cell type specific factor recognizes the rat thyroglobulin promoter.
A;Reference number: I58273; MUID:88040446; PMID:3671079
A;Accession: I58273
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-12 <RES>
A;Cross-references: UNIPROT:Q63579; EMBL:X06162; NID:957368; PIDN:CAA29519.1; PID:957369

Query Match 27.4%; Score 23; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 9.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 LWIKT 14
||: |
Db 6 LNVST 10

RESULT 9
B39109
hypothetical 1.5K protein - hepatitis C virus
N;Alternate names: hypothetical protein 2
C;Species: hepatitis C virus
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
C;Accession: B39109; JQ1585
R;Han, J.H.; Snyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A;Reference number: A39109; MUID:91156678; PMID:1705704
A;Accession: B39109
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-15 <HAN>
R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J. Gen. Virol. 73, 1521-1525, 1992
A;Title: Cloning and sequencing of the structural region and expression of putative core
A;Reference number: JQ1584; MUID:92300349; PMID:1318944
A;Accession: JQ1585
A;Molecule type: genomic RNA
A;Residues: 1-15 <KUM>
A;Experimental source: strain U.K.

Query Match 27.4%; Score 23; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PTPPL 10
| | | |
Db 7 PGPEL 11

RESULT 10
B61457
alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)
C;Species: Tetrahymena pyriformis
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999
C;Accession: B61457
R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.
J. Protozool. 36, 562-567, 1989
A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification
A;Reference number: A61457; MUID:90095986; PMID:2689637
A;Accession: B61457
A;Molecule type: protein
A;Residues: 1-15 <BAN>
C;Genetics:
A;Genetic code: SGC5

Query Match 27.4%; Score 23; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TPPL 10
| | | |
Db 6 TPPL 9

RESULT 11
G37266
Ig heavy chain C region (Py2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: G37266
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: G37266
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <RUF>

Query Match 26.2%; Score 22; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PLW 11
| | |
Db 10 PLW 12

RESULT 12
D37267
Ig heavy chain C region (Py69) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: D37267
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: D37267
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <RUF>

Query Match 26.2%; Score 22; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PLW 11
| | |
Db 10 PLW 12

RESULT 13
PT0026
calotropin DI - mudar (fragment)
C;Species: Calotropis gigantea (mudar, madar)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: PT0026
R;Bhattacharya, D.; Sengupta, A.; Sinha, N.K.
Phytochemistry 26, 633-636, 1987
A;Title: Chemical modification and amino terminal sequence of calotropin DI from Calotropis
A;Reference number: PT0026
A;Accession: PT0026
A;Molecule type: protein
A;Residues: 1-14 <BHA>
A;Cross-references: UNIPROT:P20728

C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; monom

C;Comment: This enzyme is classified as a plant cysteine protease.
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 26.2%; Score 22; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 PTPPLW 11
| | | | |
Db 3 PEYVW 8

RESULT 14
PT0037
light harvesting complex chain III/b, photosystem I - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: PT0037; PS0205
R;Uchiyama, Y.; Taugita, A.
submitted to JIPID, June 1991
A;Reference number: PS0189
A;Accession: PT0037
A;Molecule type: protein
A;Residues: 1-15 <UCH>
A;Cross-references: UNIPROT:Q7M1V1

Query Match 26.2%; Score 22; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPP 9
| | | | |
Db 4 EAAAPPPP 11

RESULT 15
C35389
urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)
C;Species: Morganella morganii
C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004
C;Accession: C35389
R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Bacteriol. 172, 3073-3080, 1990
A;Title: Morganella morganii urease: purification, characterization, and isolation of ge
A;Reference number: A35389; MUID:90264298; PMID:2345135
A;Accession: C35389
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <HUA>
A;Cross-references: UNIPROT:P17339
C;Keywords: hydrolase

Query Match 25.0%; Score 21; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPPTPP 9
| | | | |
Db 1 MQLTTP 6

Search completed: May 26, 2005, 19:41:22
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 19:23:42 ; Search time 165 Seconds
(without alignments)
46.553 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKAMPPTPLWIKTE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	27	32.1	7	1 TPFY_PACDA	P83455 pachymedusa
2	27	32.1	10	1 TMOF_AEDAE	P19425 aedes aegypti
3	27	32.1	14	2 Q96QP2	Q96QP2 homo sapien
4	26	31.0	11	2 Q9UCR1	Q9UCR1 homo sapien
5	25	29.8	12	2 Q6X7V1	Q6X7V1 canis famill
6	25	29.8	12	2 Q8KZ86	Q8KZ86 acinetobact
7	25	29.8	13	1 ECDE_LYMDI	P80941 lymantria d
8	25	29.8	14	2 Q9TEN1	Q9TEN1 anas castan
9	25	29.8	14	2 Q9TEN3	Q9TEN3 anas gracil
10	24	28.6	8	2 Q7M1V6	Q7M1V6 solanum tub
11	24	28.6	14	2 Q6SE52	Q6SE52 drosophila
12	23	27.4	10	2 Q76MK5	Q76MK5 eurypharynx
13	23	27.4	11	2 Q81V58	Q81V58 homo sapien
14	23	27.4	12	2 Q63579	Q63579 rattus norv
15	23	27.4	14	1 TAT_HV1W2	P12509 human immun
16	23	27.4	14	1 TAT_HV1Z8	P12511 human immun
17	23	27.4	14	2 Q8HR43	Q8HR43 clivia mini
18	23	27.4	14	2 Q8JDM0	Q8JDM0 human immun
19	23	27.4	14	2 Q8JDM3	Q8JDM3 human immun
20	23	27.4	14	2 Q8JDM7	Q8JDM7 human immun
21	22	26.2	11	2 Q8MAZ1	Q8MAZ1 maripa pani
22	22	26.2	11	2 Q8MAZ3	Q8MAZ3 maripa repe
23	22	26.2	11	2 Q8MB39	Q8MB39 wilsonia hu
24	22	26.2	11	2 Q8MB58	Q8MB58 seddera hir
25	22	26.2	11	2 Q8MB77	Q8MB77 odonellia h
26	22	26.2	11	2 Q8MB79	Q8MB79 antiseia arg
27	22	26.2	11	2 Q8MB97	Q8MB97 merremia pe
28	22	26.2	11	2 Q8MBE1	Q8MBE1 ipomoea alb
29	22	26.2	13	2 Q43174	Q43174 solanum tub
30	22	26.2	14	1 CALI_CALGI	P20728 calotropis
31	22	26.2	15	2 Q9T2G9	Q9T2G9 solanum tub

32	22	26.2	15	2	Q7M1V1	Q7M1V1 oryza sativ
33	22	26.2	15	2	Q9S8R4	Q9S8R4 gossypium h
34	21	25.0	6	1	E101_LITRU	P82096 litoria rub
35	21	25.0	9	2	Q9H326	Q9H326 homo sapien
36	21	25.0	9	2	Q6SP94	Q6SP94 chlamydomon
37	21	25.0	9	2	Q99193	Q99193 pseudomonas
38	21	25.0	9	2	Q9PRJ4	Q9PRJ4 lepisosteus
39	21	25.0	10	1	BRK_ONCMY	Q9PRJ1 oncorhynchus
40	21	25.0	10	1	PNAS_PRUDU	P81998 prunus dulc
41	21	25.0	10	1	URE3_MORMO	P17339 morganella
42	21	25.0	10	2	Q67BK2	Q67BK2 klebsiella
43	21	25.0	11	1	BPP_AKHP	P04562 agkistrodon
44	21	25.0	11	2	O77896	O77896 oreochromis
45	21	25.0	11	2	Q7M1W2	Q7M1W2 canavalia e

ALIGNMENTS

RESULT 1
TPFY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tryptophyllin-1 (Pdt-1).
OS Pachymedusa dactylophora (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B., Ori D.F., Shaw C.;
RT "Pachymedusa dactylophora tryptophyllin-1 (Pdt-1): structural characterization, pharmacological activity and cloning of precursor cDNA."
RL Submitted (SEP-2002) to Swiss-Prot.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI; RANGE=1-7; NOTE=Ref.1.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contractility; NAS.
KW Amidation; Amphibian defense peptide; Direct protein sequencing; Hydroxylation.
FT MOD_RES 3 3 Hydroxyproline.
FT MOD_RES 7 7 Proline amide.
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;
Query Match 32.1%; Score 27; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PPLWI 12

Db |||:

2 PPAW 6

RESULT 2

TMOF_AEDAE STANDARD; PRT; 10 AA.
AC P19425;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
 OX NCBI_TaxID=7159;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Vero beach; TISSUE=Ovary;
 RX MEDLINE=9036788; PubMed=2394318;
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
 RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like
 RT enzyme biosynthesis in the midgut.";
 RL FASEB J. 4:3015-3020(1990).
 RN [2]
 RP SEQUENCE.
 RC STRAIN=Vero beach; TISSUE=Ovary;
 RX MEDLINE=93357794; PubMed=8353526; DOI=10.1016/0965-1748(93)90044-S;
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
 RT "Mass spectrometry and characterization of Aedes aegypti trypsin
 RT modulating oostatic factor (TMOF) and its analogs.";
 RL Insect Biochem. Mol. Biol. 23:703-712(1993).
 CC -!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
 CC in the midgut which indirectly reduces the vitellogenin
 CC concentration in the hemolymph resulting in inhibition of oocyte
 CC development.
 CC -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular
 CC epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs
 CC and stops at 56 hrs.
 DR PIR: A36454; A36454.
 KW Direct protein sequencing; Hormone.
 FT DOMAIN 3 10 Poly-Pro.
 FT VARIANT 1 2 YD -> DY (in TMOF(B)).
 SQ SEQUENCE 10 AA; 1047 MW; 236D0A7777776DC7 CRC64;
 Query Match 32.1%; Score 27; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 DPTPP 9
 Db 2 DPAPP 6
 RESULT 3
 Q96QP2 ID Q96QP2 PRELIMINARY; PRT; 14 AA.
 AC Q96QP2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Tissue factor pathway inhibitor-2 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22643823; PubMed=12757776; DOI=10.1016/S0049-3848(03)00147-6;
 RA Hube F., Reverdiu P., Iochmann S., Cherpi-Antar C., Gruel Y.;
 RT "Characterization and functional analysis of TFPI-2 gene promoter in a
 RT human choriocarcinoma cell line.";
 RL Thromb. Res. 109:207-215(2003).
 DR EMBL: AY044097; AAK72693.1; -.
 FT NON TER 14
 FT NON TER 14
 SQ SEQUENCE 14 AA; 1509 MW; 4E70ED6001BC1177 CRC64;
 Query Match 32.1%; Score 27; DB 2; Length 14;
 Best Local Similarity 71.4%; Pred. No. 2.1e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 MDPTPPL 10
 Db 1 MDPARPL 7
 RESULT 4
 Q96QP2 ID Q96QP2 PRELIMINARY; PRT; 14 AA.
 AC Q96QP2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Tissue factor pathway inhibitor-2 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22643823; PubMed=12757776; DOI=10.1016/S0049-3848(03)00147-6;
 RA Hube F., Reverdiu P., Iochmann S., Cherpi-Antar C., Gruel Y.;
 RT "Characterization and functional analysis of TFPI-2 gene promoter in a
 RT human choriocarcinoma cell line.";
 RL Thromb. Res. 109:207-215(2003).
 DR EMBL: AY044097; AAK72693.1; -.
 FT NON TER 14
 FT NON TER 14
 SQ SEQUENCE 14 AA; 1509 MW; 4E70ED6001BC1177 CRC64;
 Query Match 32.1%; Score 27; DB 2; Length 14;
 Best Local Similarity 71.4%; Pred. No. 2.1e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 MDPTPPL 10
 Db 1 MDPARPL 7
 RESULT 4

Q9UCR1 ID Q9UCR1 PRELIMINARY; PRT; 11 AA.
 AC Q9UCR1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE AUTOTAXIN (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92129337; PubMed=1733949;
 RA Stracke M.L., Kruttsch H.C., Unsworth E.J., Arestad A., Cioce V.,
 RA Schiffmann E., Liotta D.A.;
 RT "Identification, purification, and partial sequence analysis of
 RT autotaxin, a novel motility-stimulating protein.";
 RL J. Biol. Chem. 267:2524-2529(1992).
 FT NON TER 1 1
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1171 MW; 2723615AA0437737 CRC64;
 Query Match 31.0%; Score 26; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 PLWI 12
 Db 4 PLWI 7
 RESULT 5
 Q6X7V1 ID Q6X7V1 PRELIMINARY; PRT; 12 AA.
 AC Q6X7V1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Insulin-like factor 3 (Fragment).
 GN Name=INSL3;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22929740; PubMed=12890727;
 RA Truong A., Bogatcheva N.V., Schelling C., Dolf G., AgoulNIK A.I.;
 RT "Isolation and expression analysis of the canine insulin-like factor 3
 RT gene.";
 RL Biol. Reprod. 69:1658-1664(2003).
 DR EMBL: AY251015; AAF79619.1; -.
 FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1354 MW; 20ED91ADFA7DD737 CRC64;
 Query Match 29.8%; Score 25; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 4 MDPTPLW 11
 Db 1 MSPRPLAW 8
 RESULT 6
 Q8KZ86 ID Q8KZ86 PRELIMINARY; PRT; 12 AA.
 AC Q8KZ86;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Class I integron DNA integrase (Fragment).

GN Name=intl1;
 OS Acinetobacter baumannii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=470;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22270987; PubMed=12384388;
 RA Gombac F., Riccio M.L., Rossolini G.M., Lagatolla C., Tonin E.,
 RA Monti-Bragadin C., Lavenia A., Dolzani L.;
 RT "Molecular characterization of integrons in epidemiologically
 RT unrelated clinical isolates of Acinetobacter baumannii from Italian
 RT hospitals reveals a limited diversity of gene cassette arrays.";
 RL Antimicrob. Agents Chemother. 46:3665-3668(2002).
 DR EMBL; AJ313334; CAC85941.1; -;
 FT NON TER 12
 SQ SEQUENCE 12 AA; 1296 MW; 90426B8F5E376DC1 CRC64;
 Query Match 29.8%; Score 25; DB 2; Length 12;
 Best Local Similarity 62.5%; Pred. No. 3.6e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 AMDPTPL 10
 Db 4 ATAPLPL 11
 RESULT 7
 ECDE LYMDI
 ID ECDE LYMDI STANDARD; PRT; 13 AA.
 AC P80941;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Testis ecdysiotropin peptide E (TE).
 OS Lymantria dispar (Gypsy moth).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 OC Lymantriidae; Lymantria.
 OX NCBI_TaxID=13123;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=97387807; PubMed=9243792;
 RX DOI=10.1002/(SICI)1520-6327(1997)36:1<37::AID-ARCH4>3.3.CO;2-3;
 RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
 RA Bell R.A.;
 RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
 RT gonadotropin isolated from brains of Lymantria dispar pupae.";
 RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
 CC -1- FUNCTION: Stimulates synthesis of ecdysteroid in the testes of
 CC larvae and pupae.
 KW Direct protein sequencing.
 SQ SEQUENCE 13 AA; 1357 MW; 1841B4CA3275B764 CRC64;
 Query Match 29.8%; Score 25; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 4e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 AMDPTP 8
 Db 2 AIDPNP 7
 RESULT 8
 Q9TEN1
 ID Q9TEN1 PRELIMINARY; PRT; 14 AA.
 AC Q9TEN1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE ATPase 8 (Fragment).
 OS Anas castanea (Chestnut teal).

OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=45631;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kennedy M., Spencer H.G.;
 RT "Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";
 RL Auk 117:154-163(2000).
 DR EMBL; AF173494; AAD51052.1; -;
 DR GO: GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1672 MW; 80FB803727F9B871 CRC64;
 Query Match 29.8%; Score 25; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 4.3e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 PTPPLW 11
 Db 6 PTPPAW 11
 RESULT 9
 Q9TEN3
 ID Q9TEN3 PRELIMINARY; PRT; 14 AA.
 AC Q9TEN3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE ATPase 8 (Fragment).
 OS Anas gracilis (Grey teal).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=45630;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kennedy M., Spencer H.G.;
 RT "Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";
 RL Auk 117:154-163(2000).
 DR EMBL; AF173493; AAD51050.1; -;
 DR GO: GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1672 MW; 80FB803727F9B871 CRC64;
 Query Match 29.8%; Score 25; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 4.3e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 PTPPLW 11
 Db 6 PTPPAW 11
 RESULT 10
 Q7M1V6
 ID Q7M1V6 PRELIMINARY; PRT; 8 AA.
 AC Q7M1V6;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Lectin (fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RA Millar D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R.,

RA Bolwell G.P.;
 RT "Chitin-binding proteins in potato (Solanum tuberosum L.) tuber.
 RT Characterization, immunolocalization and effects of wounding.";
 RL Biochem. J. 283:813-821(1992).
 DR PIR; S21288; S21288. 1
 FT NON TER 1
 FT NON TER 8
 SQ SEQUENCE 8 AA; 771 MW; C3775A71B5BDDA CRC64;

Query Match 28.6%; Score 24; DB 2; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.6e+06;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AMDPTPP 9
 Db 2 ASTPSPP 8

RESULT 11

ID Q6SE52 PRELIMINARY; PRT; 14 AA.
 AC Q6SE52;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Pgi (Fragment).
 OS Drosophila simulans (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7240;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14762063; DOI=10.1101/gr.1329204;
 RA Halligan D.L., Eyre-Walker A., Andolfatto P., Keightley P.D.;
 RT "Patterns of evolutionary constraints in intronic and intergenic DNA
 RT of Drosophila."
 RL Genome Res. 14:273-279(2004).
 DR EMBL; AY459549; AAR23007.1; -.
 FT NON TER 14
 SQ SEQUENCE 14 AA; 1456 MW; 2C83E49CCDBE7E37 CRC64;

Query Match 28.6%; Score 24; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 6.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PTPPL 10
 Db 4 PLPPL 8

RESULT 12

ID Q76MK5 PRELIMINARY; PRT; 10 AA.
 AC Q76MK5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ATPase subunit 8 (Fragment).
 GN Name=ATPase 8;
 OS Eurypharynx pelecanoides (pelican eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 OX NCBI_TaxID=55117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22967687; PubMed=12949142; DOI=10.1093/molbev/msg206;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
 RT scale gene rearrangements originated within the eels."
 RL Mol. Biol. Evol. 20:1917-1924(2003).

RA SEQUENCE FROM N.A.
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046487; BAB87160.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 10
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;

Query Match 27.4%; Score 23; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 6.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDPTP 8
 Db 4 LDPSP 8

RESULT 13

ID Q8IVG8 PRELIMINARY; PRT; 11 AA.
 AC Q8IVG8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Low density lipoprotein receptor related protein 1 (lipoprotein
 DE receptor-related protein) (Fragment).
 GN Name=LRP;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Glaeser C.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Schulz S.;
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=90089395; PubMed=2597675;
 RA Kuett H.C., Herz J., Stanley K.K.;
 RT "Structure of the low-density lipoprotein receptor-related protein
 RT (LRP) Promoter";
 RL Biochim. Biophys. Acta 1009:229-236(1989).
 DR EMBL; Y18524; CAD57169.1; -.
 DR EMBL; X15424; CAA33464.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Lipoprotein; Receptor.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1221 MW; 373D041E27273777 CRC64;

Query Match 27.4%; Score 23; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TPPL 10
 Db 3 TPPL 6

RESULT 14

Q63579 PRELIMINARY; PRT; 12 AA.
 ID Q63579
 AC Q63579;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Rat thyroglobulin gene (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8040446; PubMed=3671079;
RA Musti A.M., Ursini V.M., Avvedimento E.V., Zimarino V., Lauro R.D.;
RT "A cell type specific factor recognizes the thyroglobulin promoter.";
RL Nucleic Acids Res. 15:8149-8166(1987).
DR EMBL; X06162; CAA29519.1; -.
DR FIR; I58273; I58273.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1441 MW; D7158AD39BD37732 CRC64;

Query Match 27.4%; Score 23; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 LWIKT 14
DB 6 LWVST 10

RESULT 15
TAT_HVIW2
ID TAT_HVIW2 STANDARD; PRT; 14 AA.
AC P12509;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN Name-TAT;
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
RT at risk for AIDS."
RL Science 232:1548-1553(1986).
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter.
CC -!- SUBUNIT: Binds cyclin T1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- MISCELLANEOUS: Isolates WMJ1, WMJ2, and WMJ3 were obtained from
CC blood samples sequentially taken from a two-year old Haitian who
CC was perinatally infected by her mother.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M12507; AAB12991.1; -.
DR HSSP; P04610; 1JFW.
DR HIV; M12507; TAT\$WMJ2.
KW Activator; AIDS; Nuclear protein; RNA-binding;
KW Transcription regulation.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1467 MW; 37CC737BF6F67AAB CRC64;

Query Match 27.4%; Score 23; DB 1; Length 14;

Best Local Similarity 80.0%; Pred. No. 8.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTTP 9
DB 8 DPTGP 12

Search completed: May 26, 2005, 19:40:36
Job time : 168 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2005, 19:22:57 ; Search time 159 Seconds
(without alignments)
36.487 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKANDPTPLWKTE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	15	2 AAW11575	AAW11575 N-termina
2	84	100.0	15	2 AAW53841	AAW53841 N-terminu
3	84	100.0	15	7 ABB80223	ABB80223 Synthetic
4	69	82.1	12	7 ABB80225	ABB80225 Synthetic
5	65	77.4	11	7 ABB80226	ABB80226 Synthetic
6	54	64.3	10	2 AAW53843	AAW53843 N-terminu
7	54	64.3	10	7 ABB80222	ABB80222 Synthetic
8	50	59.5	9	7 ABB80227	ABB80227 Synthetic
9	43	51.2	8	7 ABB80228	ABB80228 Synthetic
10	41	48.8	9	6 ABR12621	ABR12621 Human can
11	41	48.8	9	6 ABR12017	ABR12017 Human can
12	41	48.8	9	6 ABR12854	ABR12854 Human can
13	41	48.8	10	6 ABR12743	ABR12743 Human can
14	41	48.8	10	6 ABR11875	ABR11875 Human can
15	41	48.8	10	6 ABR12121	ABR12121 Human can
16	41	48.8	10	6 ABR12948	ABR12948 Human can
17	41	48.8	10	6 ABR12106	ABR12106 Human can
18	41	48.8	10	6 ABR12294	ABR12294 Human can
19	41	48.8	10	6 ABR12738	ABR12738 Human can
20	41	48.8	15	6 ABR33125	ABR33125 Human can
21	41	48.8	15	6 ABR33383	ABR33383 Human can
22	41	48.8	15	6 ABR33116	ABR33116 Human can
23	41	48.8	15	6 ABR33427	ABR33427 Human can
24	41	48.8	15	6 ABR33363	ABR33363 Human can
25	38	45.2	9	2 AAW21252	AAW21252 Hydroxyme

26	37	44.0	9	6 ABR11778	ABR11778 Human can
27	37	44.0	9	6 ABR12206	ABR12206 Human can
28	37	44.0	10	6 ABR12924	ABR12924 Human can
29	37	44.0	10	8 ADO64358	ADO64358 Human 213
30	37	44.0	15	2 AAW39043	AAW39043 Peptide r
31	37	44.0	15	6 ABR33382	ABR33382 Human can
32	36	42.9	9	6 ABR12770	ABR12770 Human can
33	36	42.9	9	6 ABR12969	ABR12969 Human can
34	36	42.9	9	6 ABR12458	ABR12458 Human can
35	36	42.9	9	6 ABR12601	ABR12601 Human can
36	36	42.9	9	6 ABR12046	ABR12046 Human can
37	36	42.9	9	6 ABR12234	ABR12234 Human can
38	36	42.9	9	8 ADO72393	ADO72393 Human 213
39	36	42.9	9	8 ADO72483	ADO72483 Human 213
40	36	42.9	9	8 ADO72536	ADO72536 Human 213
41	36	42.9	9	8 ADO72664	ADO72664 Human 213
42	36	42.9	9	8 ADO72353	ADO72353 Human 213
43	36	42.9	9	8 ADO72482	ADO72482 Human 213
44	36	42.9	9	8 ADO64670	ADO64670 Human 213
45	36	42.9	9	8 ADO65216	ADO65216 Human 213

ALIGNMENTS

RESULT 1

AAW11575

ID AAW11575 standard; peptide; 15 AA.

XX AC AAW11575;

XX DT 25-MAR-2003 (revised)

XX DT 20-MAR-1997 (first entry)

XX DB N-terminal peptide from lethal toxin neutralising factor.

XX KW Lethal toxin neutralising factor; LTNP; opossum; bee toxin;

XX KW scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.

XX OS Didelphis virginiana.

XX PN US5576297-A.

XX PD 19-NOV-1996.

XX PF 22-SEP-1994; 94US-00310340.

XX PR 10-MAY-1993; 93US-00058387.

XX (LIPP/) LIPPS B V.

XX (LIPP/) LIPPS F W.

XX PI Lipps FW, Lipps BV;

XX DR WPI; 1997-011287/01.

Treatment of victims of bee or scorpion stings or plant or bacterial toxins - by admin. of lethal toxin-neutralising factor or its N-terminal peptide.

XX FS Claim 7; Col 9; 9pp; English.

The present sequence is from the N-terminus of a 68 kD protein purified from the serum of the opossum *Didelphis virginiana*. The full-length protein is a lethal toxin neutralising factor (LTNF). The use of purified LTNF or of the chemically synthesised 15mer N-terminal peptide for treating victims of bee stings, scorpion stings and bacterial or plant toxins is claimed. The patent disclosure does not provide any evidence for neutralising activity against these various toxins. There is evidence of significant neutralising activity of the opossum LTNF and the 15mer peptide against venom from snakes of the families Crotalidae, Elapidae, Hydroiidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 15 AA;

Query Match 100.0%; Score 84; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIKTE 15
 |||||
 DB 1 LKAMDPTPLWIKTE 15

RESULT 2

AAW53841

ID AAW53841 standard; peptide; 15 AA.

XX

AC AAW53841;

XX

DT 08-JUL-1998 (first entry)

XX

DE N-terminus of opossum LTNP.

XX

KW LTNP; lethal toxin neutralising factor; opossum; envenomation; therapy;
 anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
 KW histamine reaction treatment.

XX

OS Didelphis virginiana.

XX

PN US5744449-A.

XX

PD 28-APR-1998.

XX

PF 03-JUN-1996; 96US-00657163.

XX

PR 10-MAY-1993; 93US-00058387.

XX

PR 22-SEP-1994; 94US-00310340.

XX

PA (LIPP/) LIPPS B V.

XX

PA (LIPP/) LIPPS F W.

XX

PI Lipps FW, Lipps BV;

XX

DR WPI; 1998-271108/24.

XX

XX Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
 PT venom(s) from all major families of poisonous snakes.

XX

PS Claim 1; Col 11; l1pp; English.

XX

CC This sequence represents the peptide of the invention. It is a Lethal
 CC Toxin Neutralising Factor (LTNP) moiety from a 68 kDa anti-haemorrhagic
 CC protein derived from an opossum. The peptide can be used in a method for
 CC treating a victim of envenomation from a poisonous snake, preferably a
 CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
 CC is useful for the treatment of snake bites, sepsis, allergies caused by
 CC the environment and treatment of bee or scorpion stings or toxicities
 CC caused by plant or bacterial toxins. The peptide can also be used in
 CC histamine reaction treatment. The peptide can be used in envenomation
 CC treatment for a variety of snakes without prior identification of the
 CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins

SQ Sequence 15 AA;

Query Match 100.0%; Score 84; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIKTE 15
 |||||
 DB 1 LKAMDPTPLWIKTE 15

RESULT 3

ABB80223

ID ABB80223 standard; peptide; 15 AA.

XX

AC ABB80223;

XX

DT 06-NOV-2003 (first entry)

XX

DE Synthetic LTNP, LT-15.

XX

KW Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.

XX

OS Synthetic.

XX

PN WO2003060471-A2.

XX

PD 24-JUL-2003.

XX

PF 14-JAN-2003; 2003WO-US001044.

XX

PR 14-JAN-2002; 2002US-00047945.

XX

PA (LIPP/) LIPPS B V.

XX

PA (LIPP/) LIPPS F W.

XX

PI Lipps BV, Lipps FW;

XX

DR WPI; 2003-636703/60.

XX

XX Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

XX

PS Claim 3; Page 3; 24pp; English.

XX

CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 84; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIKTE 15
 |||||
 DB 1 LKAMDPTPLWIKTE 15

RESULT 4

ABB80225


```

ID  ABB80225 standard; peptide; 12 AA.
AC  ABB80225;
XX
XX
DT  06-NOV-2003 (first entry)
XX
XX  Synthetic LTNP, LT-12.
XX
XX  Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
KW  IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW  ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KW  SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW  Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW  saliva; ELISA.
XX
XX  Synthetic.
XX
XX  WO2003060471-A2.
XX
XX  24-JUL-2003.
XX
XX  14-JAN-2003; 2003WO-US001044.
XX
XX  14-JAN-2002; 2002US-00047945.
XX
XX  (LIPP/) LIPPS B V.
PA  (LIPP/) LIPPS F W.
XX
XX  Lipps BV, Lipps FW;
PI
XX  WPI; 2003-636703/60.
XX
XX  Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
PT  insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT  asthma or diabetes, by employing an ELISA on a saliva sample from a
PT  patient.
XX
XX  Claim 7; Page 4; 24pp; English.
XX
XX  The sequences given in ABB80222-28 represent lethal toxin neutralising
CC  factor (LTNP) peptides which may be used for reducing elevated levels of
CC  serum proteins selected from immunoglobulin E (IgE), nerve growth factor
CC  (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
CC  particular, the methods of the invention are useful for diagnosing and
CC  treating conditions with elevated serum IgE levels, e.g. asthma,
CC  diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
CC  arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
CC  Addison's disease or Hodgkin's disease) or depression. The efficacy of
CC  the protein may be monitored by assaying a human endogenous protein by
CC  performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
CC  sample using an anti-serum that is specific for the protein. Saliva
CC  collection is relatively non-invasive when compared to blood collection
CC  for serum. Saliva can be centrifuged immediately, whereas blood requires
CC  clotting time before centrifugation to separate serum. Saliva proteins
CC  can be assayed by a simple ELISA test, whereas an assay of proteins from
CC  serum requires a more complicated sandwich type ELISA
XX
XX  Sequence 12 AA;
SQ
Query Match 82.1%; Score 69; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LKAMDPTPLWI 12
Db 1 LKAMDPTPLWI 12
RESULT 5
ABB80226
ID ABB80226 standard; peptide; 11 AA.
XX
XX  ABB80226;
AC
XX
XX
DT  06-NOV-2003 (first entry)
XX
XX  Synthetic LTNP, LT-12.
XX
XX  Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
KW  IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW  ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KW  SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW  Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW  saliva; ELISA.
XX
XX  Synthetic.
XX
XX  WO2003060471-A2.
XX
XX  24-JUL-2003.
XX
XX  14-JAN-2003; 2003WO-US001044.
XX
XX  14-JAN-2002; 2002US-00047945.
XX
XX  (LIPP/) LIPPS B V.
PA  (LIPP/) LIPPS F W.
XX
XX  Lipps BV, Lipps FW;
PI
XX  WPI; 2003-636703/60.
XX
XX  Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
PT  insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT  asthma or diabetes, by employing an ELISA on a saliva sample from a
PT  patient.
XX
XX  Claim 7; Page 4; 24pp; English.
XX
XX  The sequences given in ABB80222-28 represent lethal toxin neutralising
CC  factor (LTNP) peptides which may be used for reducing elevated levels of
CC  serum proteins selected from immunoglobulin E (IgE), nerve growth factor
CC  (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
CC  particular, the methods of the invention are useful for diagnosing and
CC  treating conditions with elevated serum IgE levels, e.g. asthma,
CC  diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
CC  arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
CC  Addison's disease or Hodgkin's disease) or depression. The efficacy of
CC  the protein may be monitored by assaying a human endogenous protein by
CC  performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
CC  sample using an anti-serum that is specific for the protein. Saliva
CC  collection is relatively non-invasive when compared to blood collection
CC  for serum. Saliva can be centrifuged immediately, whereas blood requires
CC  clotting time before centrifugation to separate serum. Saliva proteins
CC  can be assayed by a simple ELISA test, whereas an assay of proteins from
CC  serum requires a more complicated sandwich type ELISA
XX
XX  Sequence 11 AA;
SQ
Query Match 77.4%; Score 65; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LKAMDPTPLW 11
Db 1 LKAMDPTPLW 11
RESULT 6
AAW53843
ID AAW53843 standard; peptide; 10 AA.
XX
XX  AAW53843;
AC
XX
XX  08-JUL-1998 (first entry)
XX
XX

```

DE N-terminus of opossum LTNF.
 XX LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;
 KW anti-haemorrhagic protein; Elapidae; Vipseridae; sea snake; snake bite;
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
 KW histamine reaction treatment.
 XX
 OS Didelphis virginiana.
 XX
 PN US5744449-A.
 XX
 PD 28-APR-1998.
 XX
 XX 03-JUN-1996; 96US-00657163.
 XX
 PR 10-MAY-1993; 93US-00058387.
 PR 22-SEP-1994; 94US-00310340.
 XX
 PA (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.
 XX
 PI Lipps FW, Lipps BV;
 XX
 XX WPI; 1998-271108/24.
 XX
 XX Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
 PT venom(s) from all major families of poisonous snakes.
 PT
 XX
 PS Claim 7; Col 11; lpp; English.
 XX
 CC This sequence represents the peptide of the invention. It is a Lethal
 CC Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic
 CC protein derived from an opossum. The peptide can be used in a method for
 CC treating a victim of envenomation from a poisonous snake, preferably a
 CC poisonous snake from the family of Elapidae, Vipseridae or sea snake. It
 CC is useful for the treatment of snake bites, sepsis, allergies caused by
 CC the environment and treatment of bee or scorpion stings or toxicities
 CC caused by plant or bacterial toxins. The peptide can also be used in
 CC histamine reaction treatment. The peptide can be used in envenomation
 CC treatment for a variety of snakes without prior identification of the
 CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins
 XX
 SQ Sequence 10 AA;
 Query Match 64.3%; Score 54; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.078;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTPPL 10
 DB 1 LKAMDPTPPL 10
 RESULT 7
 ABB80222
 ID ABB80222 standard; peptide; 10 AA.
 XX
 AC ABB80222;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Synthetic LTNF, LT-10.
 XX
 KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's disease; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.

XX WO2003060471-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 14-JAN-2003; 2003WO-US001044.
 XX
 PR 14-JAN-2002; 2002US-00047945.
 XX
 XX (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.
 XX
 PI Lipps BV, Lipps FW;
 XX
 XX WPI; 2003-636703/60.
 XX
 PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 XX
 PS Claim 7; Page 3; 24pp; English.
 XX
 CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IgE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 XX
 SQ Sequence 10 AA;
 Query Match 64.3%; Score 54; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.078;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTPPL 10
 DB 1 LKAMDPTPPL 10
 RESULT 8
 ABB80227
 ID ABB80227 standard; peptide; 9 AA.
 XX
 AC ABB80227;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Synthetic LTNF, LT-9.
 XX
 KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.
 XX
 PN WO2003060471-A2.
 XX

```

PD 24-JUL-2003.
XX
PF 14-JAN-2003; 2003WO-US001044.
XX
XX 14-JAN-2002; 2002US-00047945.
PR
XX (LIPPP/) LIPPS B V.
PA (LIPPP/) LIPPS F W.
XX
XX Lipps BV, Lipps FW;
PI WPI; 2003-636703/60.
XX
XX Assaying a human endogenous protein (e.g. IgG, nerve growth factor,
PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT asthma or diabetes, by employing an ELISA on a saliva sample from a
PT patient.
XX
XX Claim 7; Page 4; 24pp; English.
PS
XX The sequences given in ABB80222-28 represent lethal toxin neutralising
XX factor (LTNP) peptides which may be used for reducing elevated levels of
XX serum proteins selected from immunoglobulin E (IgE), nerve growth factor
XX (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
XX particular, the methods of the invention are useful for diagnosing and
XX treating conditions with elevated serum IgE levels, e.g. asthma,
XX diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid
XX arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
XX Addison's disease or Hodgkin's disease) or depression. The efficacy of
XX the protein may be monitored by assaying a human endogenous protein by
XX performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
XX sample using an anti-serum that is specific for the protein. Saliva
XX collection is relatively non-invasive when compared to blood collection
XX for serum. Saliva can be centrifuged immediately, whereas blood requires
XX clotting time before centrifugation to separate serum. Saliva proteins
XX can be assayed by a simple ELISA test, whereas an assay of proteins from
XX serum requires a more complicated sandwich type ELISA
XX
SQ Sequence 9 AA;
Query Match 59.5%; Score 50; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LKAMDPTPP 9
Db 1 LKAMDPTPP 9
RESULT 9
ABB80228
ID ABB80228 standard; peptide; 8 AA.
XX
AC ABB80228;
XX
XX 06-NOV-2003 (first entry)
DT
XX Synthetic LTNP, LT-8.
DE
XX Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW saliva; ELISA.
XX
XX Synthetic.
OS
XX WO2003060471-A2.
PN
XX 24-JUL-2003.
PD
XX 14-JAN-2003; 2003WO-US001044.
PF

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XX 14-JAN-2002; 2002US-00047945.
PR
XX (LIPPP/) LIPPS B V.
PA (LIPPP/) LIPPS F W.
XX
XX Lipps BV, Lipps FW;
PI WPI; 2003-636703/60.
XX
XX Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT asthma or diabetes, by employing an ELISA on a saliva sample from a
PT patient.
XX
XX Claim 7; Page 4; 24pp; English.
PS
XX The sequences given in ABB80222-28 represent lethal toxin neutralising
XX factor (LTNP) peptides which may be used for reducing elevated levels of
XX serum proteins selected from immunoglobulin E (IgE), nerve growth factor
XX (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
XX particular, the methods of the invention are useful for diagnosing and
XX treating conditions with elevated serum IgE levels, e.g. asthma,
XX diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid
XX arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
XX Addison's disease or Hodgkin's disease) or depression. The efficacy of
XX the protein may be monitored by assaying a human endogenous protein by
XX performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
XX sample using an anti-serum that is specific for the protein. Saliva
XX collection is relatively non-invasive when compared to blood collection
XX for serum. Saliva can be centrifuged immediately, whereas blood requires
XX clotting time before centrifugation to separate serum. Saliva proteins
XX can be assayed by a simple ELISA test, whereas an assay of proteins from
XX serum requires a more complicated sandwich type ELISA
XX
SQ Sequence 8 AA;
Query Match 51.2%; Score 43; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LKAMDPTP 8
Db 1 LKAMDPTP 8
RESULT 10
ABR12621
ID ABR12621 standard; peptide; 9 AA.
XX
AC ABR12621;
XX
XX 19-MAY-2003 (first entry)
DT
XX Human cancer-related protein 156P1D4 HLA peptide #856.
DE
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.
KW
XX Homo sapiens.
OS
XX WO200283921-A2.
PN
XX 24-OCT-2002.
PD
XX 10-APR-2002; 2002WO-US011654.
PF
XX 10-APR-2001; 2001US-0282739P.
PR
XX 10-APR-2001; 2001US-0283112P.
PR
XX 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX

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CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

SQ Sequence 9 AA;

Query Match 48.8%; Score 41; DB 6; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDPTPLWI 12
 |||: |||
 Db 1 MDPSVPIWI 9

RESULT 13
 ABR12743
 ID ABR12743 standard; peptide; 10 AA.

XX AC ABR12743;

XX AC 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 156P1D4 HLA peptide #978.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.

XX OS Homo sapiens.

XX FN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US011654.

XX PR 10-APR-2001; 2001US-0282739P.

XX PR 10-APR-2001; 2001US-0283112P.

XX PR 25-APR-2001; 2001US-0286630P.

XX FA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

XX PS Claim 13; Page 239; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX SQ Sequence 10 AA;

Query Match 48.8%; Score 41; DB 6; Length 10;
 Best Local Similarity 66.7%; Pred. No. 9;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDPTPLWI 12
 |||: |||
 Db 1 MDPSVPIWI 9

RESULT 14

ABR11875

ID ABR11875 standard; peptide; 10 AA.

XX AC ABR11875;

XX AC 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 156P1D4 HLA peptide #110.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.

XX OS Homo sapiens.

XX FN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US011654.

XX PR 10-APR-2001; 2001US-0282739P.

XX PR 10-APR-2001; 2001US-0283112P.

XX PR 25-APR-2001; 2001US-0286630P.

XX FA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

XX PS Claim 13; Page 231; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX SQ Sequence 10 AA;

Query Match 48.8%; Score 41; DB 6; Length 10;
 Best Local Similarity 66.7%; Pred. No. 9;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDPTPLWI 12
 |||: |||
 Db 2 MDPSVPIWI 10

RESULT 15

ABR12121

ID ABR12121 standard; peptide; 10 AA.

XX

AC ABR12121;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 156PID4 HLA peptide #356.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 233; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 10 AA;
Query Match 48.8%; Score 41; DB 6; Length 10;
Best-Local Similarity 66.7%; Pred. No. 9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 MDPTPLWI 12
Db 1 MDPSPFIWI 9
||||:|:|

Search completed: May 26, 2005, 19:37:43
Job time : 161 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 19:40:44 ; Search time 134 Seconds
(without alignments)
38.616 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKAMDPTPLWIKTE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 258160

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	15	14	US-10-047-945-2
2	69	82.1	12	14	US-10-047-945-4
3	65	77.4	11	14	US-10-047-945-5
4	54	64.3	10	14	US-10-047-945-1
5	50	59.5	9	14	US-10-047-945-6
6	43	51.2	8	14	US-10-047-945-7
7	38	45.2	9	17	US-10-930-300-52
8	37	44.0	15	14	US-10-161-791-444
9	34	40.5	12	14	US-10-286-457-239
10	34	40.5	12	16	US-10-327-598-735
11	33	39.3	9	15	US-10-057-4758-10923
12	33	39.3	9	15	US-10-154-884B-10923
13	33	39.3	13	15	US-10-468-370-501

14	33	39.3	13	15	US-10-468-370-502	Sequence 502, App
15	33	39.3	13	16	US-10-468-496-457	Sequence 457, App
16	33	39.3	13	16	US-10-468-496-458	Sequence 458, App
17	32	38.1	12	14	US-10-185-815-6	Sequence 6, Appli
18	32	38.1	12	14	US-10-161-791-252	Sequence 252, Appli
19	32	38.1	12	15	US-10-116-275-52	Sequence 52, Appli
20	32	38.1	13	10	US-09-966-782A-27	Sequence 27, Appli
21	32	38.1	13	14	US-10-254-905-27	Sequence 13, Appli
22	32	38.1	14	9	US-09-845-583-13	Sequence 70, Appli
23	32	38.1	14	14	US-10-162-497-70	Sequence 160, App
24	32	38.1	14	17	US-10-437-708-160	Sequence 160, App
25	32	38.1	14	17	US-10-418-032-160	Sequence 188, App
26	31	36.9	9	16	US-10-611-440-188	Sequence 188, App
27	31	36.9	13	15	US-10-437-708-24	Sequence 24, Appli
28	31	36.9	13	15	US-10-437-708-198	Sequence 198, App
29	31	36.9	13	15	US-10-395-402-24	Sequence 24, Appli
30	31	36.9	13	17	US-10-418-032-24	Sequence 24, Appli
31	31	36.9	13	17	US-10-418-032-198	Sequence 198, App
32	31	36.9	14	10	US-09-932-613-192	Sequence 192, App
33	31	36.9	14	10	US-09-932-613-225	Sequence 225, App
34	31	36.9	14	10	US-09-932-322-192	Sequence 192, App
35	31	36.9	14	10	US-09-932-322-225	Sequence 225, App
36	31	36.9	15	14	US-10-282-960-53	Sequence 53, Appli
37	30	35.7	8	15	US-10-437-708-168	Sequence 168, App
38	30	35.7	8	17	US-10-418-032-168	Sequence 168, App
39	30	35.7	10	14	US-10-190-082-480	Sequence 480, App
40	30	35.7	10	15	US-10-437-708-165	Sequence 165, App
41	30	35.7	10	17	US-10-418-032-165	Sequence 165, App
42	30	35.7	12	9	US-09-995-804A-4	Sequence 4, Appli
43	30	35.7	12	14	US-10-225-567A-2288	Sequence 2288, App
44	30	35.7	13	15	US-10-437-708-21	Sequence 21, Appli
45	30	35.7	13	15	US-10-437-708-22	Sequence 22, Appli

ALIGNMENTS

RESULT 1

US-10-047-945-2
; Sequence 2, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED.
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-2

Query Match 100.0%; Score 84; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWIKTE 15

Db 1 LKAMDPTPLWIKTE 15

RESULT 2
US-10-047-945-4
; Sequence 4, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.
US-10-047-945-4

Query Match 82.1%; Score 69; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTPLWI 12
| | | | | | | | | | | | | |
Db 1 LKAMDPTPLWI 12

RESULT 3
US-10-047-945-5
; Sequence 5, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.
US-10-047-945-5

Query Match 77.4%; Score 65; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTPLW 11
| | | | | | | | | | | |
Db 1 LKAMDPTPLW 11

RESULT 4
US-10-047-945-1
; Sequence 1, Application US/10047945

; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-1

Query Match 64.3%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTPPL 10
| | | | | | | | | | | |
Db 1 LKAMDPTPPL 10

RESULT 5
US-10-047-945-6
; Sequence 6, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.
US-10-047-945-6

Query Match 59.5%; Score 50; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTPP 9
| | | | | | | | | |
Db 1 LKAMDPTPP 9

RESULT 6
US-10-047-945-7
; Sequence 7, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:

APPLICANT: LIPPS, BINIE V.
APPLICANT: LIPPS, FREDERICK W.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
FILE REFERENCE: FWLPAT015US
CURRENT APPLICATION NUMBER: US/10/047,945
CURRENT FILING DATE: 2002-01-14
PRIOR FILING DATE:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
SEQ ID NO 7
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
US-10-047-945-7

Query Match 51.2%; Score 43; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDTP 8
Db 1 LKAMDTP 8

RESULT 7
US-10-930-300-52
Sequence 52, Application US/10930300
Publication No. US20050014138A1
GENERAL INFORMATION:
APPLICANT: Rath, Matthias
TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL
OLIGOPEPTIDES
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: INHOUSE IP MANAGEMENT
STREET: 280 Colorado Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.50 inch, 1.44MB Storage
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: MS WORD 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/930,300
FILING DATE: 30-Aug-2004
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,248
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ALI KAMAREI
REGISTRATION NUMBER: 37000
REFERENCE/DOCKET NUMBER: 10262-1US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-322-7371
TELEFAX: 650-322-7389
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-930-300-52

Query Match 45.2%; Score 38; DB 17; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPPLW 11
Db 1 DPTMPLW 7

RESULT 8
US-10-161-791-444
Sequence 444, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 444:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-444

Query Match 44.0%; Score 37; DB 14; Length 15;
Best Local Similarity 66.7%; Pred. No. 99;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTPL 10
Db 5 RALPPTPL 13

RESULT 9
US-10-286-457-239
Sequence 239, Application US/10286457
Publication No. US20030166004A1

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; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 239
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-239

Query Match          40.5%; Score 34; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      8 PPLWKTE 15
      ||| |::|
Db      3 PPTWLQTK 10

RESULT 10
US-10-327-598-735
; Sequence 735, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 735
; LENGTH: 12
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-735

Query Match          40.5%; Score 34; DB 16; Length 12;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 KAMDPTPP 9
      :-|||
Db      1 QSFDP 8

RESULT 11
US-10-057-475B-10923
; Sequence 10923, Application US/10057475B
; Publication No. US2004002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
```

```
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10923
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Lyl484 short MHC HLA A2 class I binding peptide
US-10-057-475B-10923

Query Match          39.3%; Score 33; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 PPLWIKT 14
      ||| |::|
Db      3 PPLWNRT 9

RESULT 12
US-10-154-884B-10923
; Sequence 10923, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
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; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10923
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Lyl484 short MHC HLA A2 class I binding peptide
US-10-154-884B-10923

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Query Match      39.3%; Score 33; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      8 PPLWIKT 14
      ||||| :|
Db      3 PPLNWT 9

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RESULT 13
US-10-468-370-501
; Sequence 501, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 501
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-501

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Query Match      39.3%; Score 33; DB 15; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      7 TPPLWIKT 14
      ||||| :|
Db      4 TSPTWLKT 11

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RESULT 14
US-10-468-370-502
; Sequence 502, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 502
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-502

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```

Query Match      39.3%; Score 33; DB 15; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      7 TPPLWIKT 14
      ||||| :|
Db      1 TSPTWLKT 8

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RESULT 15
US-10-468-496-457
; Sequence 457, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; FILE REFERENCE: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6

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; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-457

Query Match      39.3%; Score 33; DB 16; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      7 TPPLWIKT 14
      | | | | |
Db      4 TSPTWLKT 11
```

Search completed: May 26, 2005, 19:53:55
Job time : 159 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2005, 19:32:43 ; Search time 43 Seconds
(without alignments)
26.040 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKAMDPTPLWKITE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 164526

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	15	1	US-08-310-340A-1
2	84	100.0	15	1	US-08-657-163A-1
3	54	64.3	10	1	US-08-657-163A-2
4	37	44.0	15	3	US-08-602-999A-444
5	37	44.0	15	4	US-09-500-124-444
6	32	38.1	11	1	US-08-336-343A-31
7	32	38.1	11	3	US-08-652-877-31
8	32	38.1	11	3	US-08-476-515A-31
9	32	38.1	12	3	US-08-602-999A-252
10	32	38.1	12	4	US-09-500-124-252
11	32	38.1	14	3	US-08-268-992-70
12	32	38.1	14	3	US-09-657-474-70
13	32	38.1	14	4	US-08-845-583A-13
14	32	38.1	14	4	US-08-547-693-160
15	31	36.9	13	3	US-08-232-446B-11
16	31	36.9	13	4	US-08-119-507B-24
17	31	36.9	13	4	US-08-897-556A-24
18	31	36.9	13	4	US-09-547-693-24
19	31	36.9	13	4	US-09-547-693-198
20	30	35.7	6	3	US-08-232-446B-24
21	30	35.7	10	4	US-09-547-693-168
22	30	35.7	8	4	US-08-547-693-165
23	30	35.7	12	2	US-08-659-984A-8
24	30	35.7	12	3	US-08-660-531-8
25	30	35.7	12	4	US-08-995-804B-4
26	30	35.7	12	4	US-08-119-507B-21
27	30	35.7	13	4	US-09-119-507B-22

28	30	35.7	13	4	US-09-119-507B-23
29	30	35.7	13	4	US-08-897-556A-21
30	30	35.7	13	4	US-08-897-556A-22
31	30	35.7	13	4	US-08-897-556A-23
32	30	35.7	13	4	US-09-547-693-21
33	30	35.7	13	4	US-09-547-693-22
34	30	35.7	13	4	US-09-547-693-23
35	30	35.7	13	4	US-09-547-693-195
36	30	35.7	13	4	US-09-547-693-197
37	30	35.7	14	2	US-08-687-956A-4
38	30	35.7	14	2	US-08-659-984A-11
39	30	35.7	14	3	US-08-660-531-11
40	30	35.7	14	4	US-09-547-693-196
41	29	34.5	15	4	US-09-148-712-24
42	29	34.5	12	4	US-09-315-926A-18
43	29	34.5	15	1	US-08-185-432-11
44	29	34.5	15	3	US-08-602-999A-385
45	29	34.5	15	3	US-08-602-999A-452

ALIGNMENTS

RESULT 1

US-08-310-340A-1

; Sequence 1, Application US/08310340A

; Patent No. 5576297

; GENERAL INFORMATION:

; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS

; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND

; TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR

; TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BINIE V. LIPPS

; STREET: 4509 MIMOSA DR.

; CITY: BELLAIRE

; STATE: TEXAS

; COUNTRY: USA

; ZIP: 77401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB

; COMPUTER: IBM COMPATIBLE

; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1

; SOFTWARE: MS WORD 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/310,340A

; FILING DATE: 22 SEPTEMBER 1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/058, 387

; FILING DATE: 10 MAY 1993

; ATTORNEY/AGENT INFORMATION:

; NAME:

; REGISTRATION NUMBER:

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 713-723-6845

; TELEFAX: 713-663-7290

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15

; TYPE: AMINO ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N

; ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:

; ORGANISM: DIDELPHIS VIRGINIANA

; STRAIN: WILD

INDIVIDUAL ISOLATE: TEXAS WILD
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1;
LIBRARY:
CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
VOLUME: SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
US-08-310-340A-1
Query Match 100.0%; Score 84; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTPLWKTE 15
Db 1 LKAMDPTPLWKTE 15
RESULT 2
US-08-657-163A-1
Sequence 1, Application US/08657163A
Patent No. 5744449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LTNFS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
TELEX:
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA; SEQ ID NO: 1;
ORGANISM: DIDELPHIS VIRGINIANA
STRAIN: WILD
INDIVIDUAL ISOLATE: TEXAS WILD
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1;
LIBRARY:
CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
US-08-657-163A-1
Query Match 100.0%; Score 84; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTPLWKTE 15
Db 1 LKAMDPTPLWKTE 15
RESULT 3
US-08-657-163A-2
Sequence 2, Application US/08657163A
Patent No. 5744449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LTNFS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514

```
; APPLICATION NUMBER: 08/058,387
; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN R. CASPERSON
; REGISTRATION NUMBER: 28,198
; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-482-2961
; TELEFAX: 713-663-7290
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N
; ORIGINAL SOURCE: SYNTHETIC
; US-08-657-163A-2

Query Match 64.3%; Score 54; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10
   :|: |||||
Db 1 LKAMDPTPPL 10

RESULT 4
US-08-602-999A-444
; Sequence 444, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 444:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-444

Query Match 44.0%; Score 37; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTPPL 10
   :|: |||||
Db 5 RALPPTPPL 13

RESULT 5
US-09-500-124-444
; Sequence 444, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 444:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-444

Query Match 44.0%; Score 37; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTPPL 10
   :|: |||||
Db 5 RALPPTPPL 13
```

```
; APPLICATION NUMBER: 08/058,387
; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN R. CASPERSON
; REGISTRATION NUMBER: 28,198
; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-482-2961
; TELEFAX: 713-663-7290
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N
; ORIGINAL SOURCE: SYNTHETIC
; US-08-657-163A-2

Query Match 64.3%; Score 54; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10
   :|: |||||
Db 1 LKAMDPTPPL 10

RESULT 4
US-08-602-999A-444
; Sequence 444, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 444:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-444

Query Match 44.0%; Score 37; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTPPL 10
   :|: |||||
Db 5 RALPPTPPL 13

RESULT 5
US-09-500-124-444
; Sequence 444, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 444:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-444

Query Match 44.0%; Score 37; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTPPL 10
   :|: |||||
Db 5 RALPPTPPL 13
```

RESULT 6
US-08-336-343A-31
; Sequence 31, Application US/08336343A
; Patent No. 5677144
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Alves, Frauke
; TITLE OF INVENTION: CKK-2, A No. 5677144el Receptor Tyrosine Kinase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,343A
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-336-343A-31

Query Match 38.1%; Score 32; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPPL 10
| | | | |
DB 3 KMPRPPL 11

RESULT 7
US-08-652-877-31
; Sequence 31, Application US/08652877
; Patent No. 6187548
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjalms, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd., 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.5.1
; SOFTWARE: Word 6.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,877
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15203
; FILING DATE: 22-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,314
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355E-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-652-877-31

Query Match 38.1%; Score 32; DB 3; Length 11;
Best Local Similarity 66.7%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPPL 10
| | | | |
DB 3 KMPRPPL 11

RESULT 8
US-08-476-515A-31
; Sequence 31, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjalms, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
; STREET: 3C43,
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/476,515A
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/344,836
;; FILING DATE: 23-NOV-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/SE94/00483
;; FILING DATE: 24-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: SE 9301764-8
;; FILING DATE: 24-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Savitzky, Martin
;; REGISTRATION NUMBER: 29,699
;; REFERENCE/DOCKET NUMBER: A1355D
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-454-3816
;; TELEFAX: 610-454-3816
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHEetical: NO
;; FRAGMENT TYPE: internal
US-08-476-515A-31

Query Match 38.1%; Score 32; DB 3; Length 11;
Best Local Similarity 66.7%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KAMDPTPPL 10
Db 3 KMPPPRPPL 11

RESULT 9
US-08-602-999A-252
;; Sequence 252, Application US/08602999A
;; Patent No. 6184205
;; GENERAL INFORMATION:
;; APPLICANT: SPARKS, Andrew B.
;; APPLICANT: KAY, Brian K.
;; APPLICANT: THORN, Judith M.
;; APPLICANT: QUILLIAM, Lawrence A.
;; APPLICANT: DER, Channing J.
;; APPLICANT: FOWLKES, Dana M.
;; APPLICANT: RIDER, James E.
;; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;; TITLE OF INVENTION: ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 467
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/602,999A
;; FILING DATE: 16-FEB-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Misrock, S. Leslie

;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 252:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-602-999A-252

Query Match 38.1%; Score 32; DB 3; Length 12;
Best Local Similarity 66.7%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KAMDPTPPL 10
Db 4 KMPPPRPPL 12

RESULT 10
US-09-500-124-252
;; Sequence 252, Application US/09500124
;; Patent No. 6432920
;; GENERAL INFORMATION:
;; APPLICANT: SPARKS, Andrew B.
;; APPLICANT: KAY, Brian K.
;; APPLICANT: THORN, Judith M.
;; APPLICANT: QUILLIAM, Lawrence A.
;; APPLICANT: DER, Channing J.
;; APPLICANT: FOWLKES, Dana M.
;; APPLICANT: RIDER, James E.
;; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;; TITLE OF INVENTION: ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 467
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/500,124
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Misrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 252:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-09-500-124-252

Query Match 38.1%; Score 32; DB 4; Length 12;
Best Local Similarity 66.7%; Pred. NO. 88;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDTPPL 10
| | | | |
Db 4 KMPRPPL 12

RESULT 11
US-09-268-992-70
; Sequence 70, Application US/09268992
; Patent No. 6342351
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; AND TREATING CHROMOSOME-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; CURRENT FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: 09/236,134
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-268-992-70

Query Match 38.1%; Score 32; DB 3; Length 14;
Best Local Similarity 80.0%; Pred. NO. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 TPPLW 11
| | | | |
Db 7 TPPIW 11

RESULT 12
US-09-657-474-70
; Sequence 70, Application US/09657474
; Patent No. 6399762
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; AND TREATING CHROMOSOME-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/657,474
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 14
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-657-474-70

Query Match 38.1%; Score 32; DB 3; Length 14;
Best Local Similarity 80.0%; Pred. NO. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 TPPLW 11
| | | | |
Db 7 TPPIW 11

RESULT 13
US-09-845-583A-13
; Sequence 13, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champilaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583A-13

Query Match 38.1%; Score 32; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. NO. 1e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 AMDPTPLWI 12
| | | | |
Db 2 ANSPRDLWV 11

RESULT 14
US-09-547-693-160
; Sequence 160, Application US/09547693
; Patent No. 6639050
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; Glycoproteins
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/09/547,693
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 160
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
; NAME/KEY: SITE
; LOCATION: (3)..(3)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; NAME/KEY: SITE
; LOCATION: (7)..(7)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; NAME/KEY: SITE
; LOCATION: (9)..(10)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.

```
; NAME/KEY: SITE
; LOCATION: (14)...(14)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
US-09-547-693-160

Query Match      38.1%; Score 32; DB 4; Length 14;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      3 AMDPTPPL 10
      : : |||||
Db      4 SLTPTPPL 11

RESULT 15
US-09-232-446B-11
; Sequence 11, Application US/09232446B
; Patent No. 6228647
; GENERAL INFORMATION:
; APPLICANT: Voytas, Daniel F.
; APPLICANT: Gal, Xiaowu
; TITLE OF INVENTION: Transposable Element Protein that Directs DNA
; TITLE OF INVENTION: Integration to Specific Chromosomal Sites
; FILE REFERENCE: 2-98
; CURRENT APPLICATION NUMBER: US/09/232,446B
; CURRENT FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 60/071,383
; PRIOR FILING DATE: 1998-01-15
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mutant peptide
; OTHER INFORMATION: sequence
US-09-232-446B-11

Query Match      36.9%; Score 31; DB 3; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      3 AMDPTPP 9
      : : |||
Db      4 SLDPSP 10

Search completed: May 26, 2005, 19:42:09
Job time : 44 secs
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 19:51:16 ; Search time 38 Seconds
(without alignments)
12.660 Million cell updates/sec

Title: US-10-047-945-3

Perfect score: 24

Sequence: 1 LKAMD 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	45.8	4	2	151049
2	11	45.8	5	2	A32516
3	11	45.8	5	2	B31836
4	9	37.5	4	2	A48360
5	9	37.5	4	2	PL0146
6	9	37.5	4	2	JQ1273
7	9	37.5	5	2	B41225
8	9	37.5	5	2	PT0624
9	9	37.5	5	2	PT0651
10	8	33.3	5	2	S5237
11	7	29.2	3	3	S13894
12	7	29.2	4	2	A61300
13	7	29.2	4	2	I40870
14	7	29.2	4	2	T46627
15	7	29.2	4	2	E44823
16	7	29.2	4	2	I57745
17	7	29.2	4	2	I40804
18	6	25.0	3	3	PT0578
19	6	25.0	4	2	S18401
20	6	25.0	4	2	A41890
21	6	25.0	4	2	S43014
22	6	25.0	4	2	D41654
23	6	25.0	4	2	B53284
24	6	25.0	4	2	S47552
25	6	25.0	4	2	A26209
26	6	25.0	4	2	I40697
27	6	25.0	4	2	A35779
28	6	25.0	4	2	A32480
29	6	25.0	4	2	PT0271

30 6 25.0 4 2 PT0696 T-cell receptor be
31 6 25.0 4 2 PT0711 T-cell receptor be
32 6 25.0 5 2 JN0860 peptidyl-dipeptida
33 6 25.0 5 2 S70154 URF2 protein - Xan
34 6 25.0 5 2 B60274 major protein anti
35 6 25.0 5 2 D60274 major protein anti
36 6 25.0 5 2 S70615 endo-1,4-beta-xyla
37 6 25.0 5 2 PQ0009 angiotensin-conver
38 6 25.0 5 2 PQ0689 photosystem I 10.4
39 6 25.0 5 2 A60803 neuropeptide - sea
40 6 25.0 5 2 PT0267 Ig heavy chain CRD
41 6 25.0 5 2 PT0281 Ig heavy chain CRD
42 6 25.0 5 2 PT0308 Ig heavy chain CRD
43 6 25.0 5 2 PT0596 T-cell receptor be
44 6 25.0 5 2 PT0513 T-cell receptor be
45 6 25.0 5 2 PT0729 T-cell receptor be

ALIGNMENTS

RESULT 1

I51049

metallothionein-A - rainbow trout (fragment)

C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C;Accession: I51049

R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.

Eur. J. Biochem. 230, 344-349, 1995

A;Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) me-

A;Reference number: I51049; MUID:95324545; PMID:7601121

A;Accession: I51049

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-4 <OLS>

A;Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 45.8%; Score 11; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MD 5

Db 1 MD 2

RESULT 2

A32516

cholecystokinin-5 - dog

N;Alternate names: CCK-5

C;Species: Canis lupus familiaris (dog)

C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000

C;Accession: A32516

R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.

Am. J. Physiol. 252, G272-G275, 1987

A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intest-

A;Reference number: A32516; MUID:87153871; PMID:3826354

A;Accession: A32516

A;Molecule type: protein

A;Residues: 1-5 <SHI>

C;Comment: This peptide

C;Superfamily: gastrin

C;Keywords: amidated carboxyl end; neuropeptide

F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 45.8%; Score 11; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MD 5

Db 3 MD 4

cholecysto

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RESULT 3
B31836
20K protein - Rickettsia rickettsii (fragment)
C:Species: Rickettsia rickettsii
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
C:Accession: B31836
R:Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
J. Bacteriol. 170, 4493-4500, 1988
A:Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii
A:Reference number: A91885; MUID:89008059; PMID:3139629
A:Accession: B31836
A:Molecule type: DNA
A:Residues: 1-5 <AND>
A:Cross-references: GB:J03371; NID:g152455; PIDN:AAD15030.1; PID:g4262874

Query Match 45.8%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MD 5
DB 1 MD 2

RESULT 4
A48360
gamma subunit of Protein A - Methylosinus trichosporium (fragment)
C:Species: Methylosinus trichosporium
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A48360
R:Cardy, D.L.; Laidler, V.; Salmond, G.P.; Murrell, J.C.
Arch. Microbiol. 156, 477-483, 1991
A:Title: The methane monooxygenase gene cluster of Methylosinus trichosporium: cloning a
A:Reference number: A48360; MUID:92153031; PMID:1785954
A:Contents: OB3b
A:Accession: A48360
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <CAR>
A:Cross-references: GB:S81887; NID:g245213; PIDN:AAB21391.1; PID:g245214
A:Note: sequence extracted from NCBI backbone (NCBIN:81887, NCBIP:81912)

Query Match 37.5%; Score 9; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKA 3
DB 2 LQA 4

RESULT 5
P10146
carbon-monoxide dehydrogenase (EC 1.2.99.2) small chain - Pseudomonas carboxydohydrogena
C:Species: Pseudomonas carboxydohydrogena
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: P10146
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydohydrogena
A:Reference number: P10138; MUID:90055878; PMID:2818128
A:Accession: P10146
A:Molecule type: protein
A:Residues: 1-4 <KGA>
A:Cross-references: UNIPROT:P19918
A:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, medium, and small
C:Keywords: oxidoreductase

Query Match 37.5%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 KA 3
DB 3 KA 4

RESULT 6
JQ1273
neuropeptide Antho-Kamide - sea anemone (Anthopleura elegantissima)
C:Species: Anthopleura elegantissima
C:Date: 31-Mar-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: JQ1273
R:Nothacker, H.P.; Rinehart, K.L.; Grimmelikhuijzen, C.J.P.
Biochem. Biophys. Res. Commun. 179, 1205-1211, 1991
A:Title: Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropeptide
A:Reference number: JQ1273; MUID:92028852; PMID:1681803
A:Accession: JQ1273
A:Molecule type: protein
A:Residues: 1-4 <NOT>
A:Cross-references: UNIPROT:P58705
C:Comment: The carboxyl-terminal amide probably arises from cleavage of a following glycine
C:Keywords: amidated carboxyl end; neuropeptide; phenyllactylation
F:1/Modified site: L-3-phenyllactic acid (Phe) #status experimental
F:4/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match 37.5%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KA 3
DB 3 KA 4

RESULT 7
B41225
copper resistance protein B - Pseudomonas syringae pv. tomato (fragment)
C:Species: Pseudomonas syringae pv. tomato
C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C:Accession: B41225
R:Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A:Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer membrane
A:Reference number: A41225; MUID:92020961; PMID:1924351
A:Accession: B41225
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <CHA>

Query Match 37.5%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AM 4
DB 4 AM 5

RESULT 8
PT0624
T-cell receptor beta chain V-D-J region (120-1K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0624
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Functional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0624
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

```

Query Match 37.5%; Score 9; DB 2; Length 5;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AMD 5
 Db 3 SLD 5

RESULT 9
 PT0651
 T-cell receptor beta chain V-D-J region (121-1C) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0651
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0651
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <PEE>
 A:Experimental source: day 4 postnatal thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 37.5%; Score 9; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AMD 5
 Db 3 ASD 5

RESULT 10
 S55237
 zinc-binding protein ZBP14 - maize (fragment)
 C:Species: Zea mays (maize)
 C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
 C:Accession: S55237
 R:Robinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A.
 Biochem. J. 307, 267-272, 1995
 A:Title: Expression and characterization of maize ZBP14, a member of a new family of zinc-binding proteins
 A:Reference number: S55237; MUID:95234046; PMID:7717986
 A:Accession: S55237
 A:Molecule type: protein
 A:Residues: 1-5 <ROB>

Query Match 33.3%; Score 8; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAM 4
 Db 1 LAAY 4

RESULT 11
 S13894
 histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
 C:Species: Brassica oleracea (wild cabbage)
 C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C:Accession: S13894
 R:Nagai, A.; Scheidegger, A.
 Arch. Biochem. Biophys. 284, 127-132, 1991
 A:Title: Purification and characterization of histidinol dehydrogenase from cabbage.
 A:Reference number: S13894; MUID:91112783; PMID:1989490
 A:Accession: S13894
 A:Molecule type: protein
 A:Residues: 1-3 <NAG>
 A:Experimental source: var. capitata

C:Keywords: dimer; NAD; oxidoreductase

Query Match 29.2%; Score 7; DB 3; Length 3;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LK 2
 Db 2 MK 3

RESULT 12

A61300

22K superhelical DNA-binding protein - Escherichia coli (fragment)

C:Species: Escherichia coli

C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999

C:Accession: A61300

R:Kishi, F.; Ebina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.

J. Biochem. 92, 1059-1068, 1982

A:Title: Purification and characterization of a protein from Escherichia coli which forms

A:Reference number: A61300; MUID:83082696; PMID:6294066

A:Accession: A61300

A:Molecule type: protein

A:Residues: 1-4 <KIS>

A:Comment: This protein resembles some of the histone-like protein of bacteria in amino

C:Keywords: DNA binding; monomer

Query Match 29.2%; Score 7; DB 2; Length 4;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MD 5
 Db 1 ME 2

RESULT 13

I40870

phospholipase C (EC 3.1.4.3) - Clostridium perfringens (fragment)

C:Species: Clostridium perfringens

C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 21-Jul-2000

C:Accession: I40870

R:Toyonaga, T.; Matsushita, O.; Katayama, S.; Minami, J.; Okabe, A.

Microbiol. Immunol. 36, 603-613, 1992

A:Title: Role of the upstream region containing an intrinsic DNA curvature in the negative

A:Reference number: I40870; MUID:92396045; PMID:1522810

A:Accession: I40870

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-4 <RES>

A:Cross-references: EMBL:X62825; NID:g40622; PIDN:CAA44636.1; PID:g4377417

C:Genetics:

A:Gene: plc

C:Keywords: phosphoric diester hydrolase

Query Match 29.2%; Score 7; DB 2; Length 4;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LK 2
 Db 1 MK 2

RESULT 14

T46627

hypothetical protein c4 - loblolly pine

C:Species: Pinus taeda (loblolly pine)

C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C:Accession: T46627

R:Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.

submitted to the EMBL Data Library, July 1995

A:Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do-

A:Reference number: Z23105
A:Accession: T46627
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4 <CHA>
A:Cross-References: EMBL:U31309; NID:g974285; PID:g974292
A:Experimental source: strain s6PT2xs6PT3; 8 month seedlings

Query Match 29.2%; Score 7; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LK 2
|
Db 1 MK 2

RESULT 15
E44823
synaptosomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)
N:Alternate names: superprotein peptide 1
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C:Accession: E44823
R:Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A:Reference number: A44823; MUID:92044785; PMID:1941090
A:Accession: E44823
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <LOE>
A:Experimental source: visual tissue
A>Note: sequence extracted from NCBI backbone (NCBIP:64247)
C:Keywords: membrane trafficking

Query Match 29.2%; Score 7; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MD 5
|
Db 2 ME 3

Search completed: May 26, 2005, 20:00:40
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 19:42:15 ; Search time 165 Seconds
(without alignments)
15.518 Million cell updates/sec

Title: US-10-047-945-3
Perfect score: 24
Sequence: 1 LKAMD 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 53

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	37.5	4	1	DCMS_PSECH
2	9	37.5	4	1	PFKA_ATEL
3	9	37.5	4	2	Q08433
4	7	29.2	3	1	LUXE_VIBFI
5	7	29.2	4	1	ILME_SEPOP
6	7	29.2	5	1	RE11_LITRU
7	7	29.2	5	2	P83073
8	6	25.0	4	1	ACH1_ACHFU
9	6	25.0	4	1	FAR3_HIRME
10	6	25.0	4	1	FLRF_HIRME
11	6	25.0	4	1	FLRN_ATEL
12	6	25.0	4	1	OCPI_OCTMI
13	6	25.0	4	1	OCPI_OCTMI
14	6	25.0	4	2	Q16047
15	6	25.0	5	1	BIOA_CITFR
16	6	25.0	5	1	FARP_CHICK
17	6	25.0	5	1	MPA4_JUNVI
18	6	25.0	5	1	TRM3_ECOLI
19	6	25.0	5	1	UKA4_CHLTR
20	5	20.8	3	1	GRWM_HUMAN
21	5	20.8	4	1	DCML_PSECH
22	5	20.8	4	1	FAR4_HIRME
23	5	20.8	4	1	FMRF_MACNI
24	5	20.8	4	1	TUFT_HUMAN
25	5	20.8	4	2	Q96A70
26	5	20.8	5	1	BIOB_CITFR
27	5	20.8	5	1	BPP7_BOTIN
28	5	20.8	5	1	BI03_LITRU
29	5	20.8	5	2	Q99007
30	4	16.7	5	1	AL14_CARMA
31	4	16.7	5	1	AP21_EISFO

32	4	16.7	5	1	FARP_ARTTR
33	4	16.7	5	1	PRCT_CARMA
34	4	16.7	5	1	PRCT_LIMPO
35	4	16.7	5	1	PRCT_PERAM
36	4	16.7	5	1	RE21_LITRU
37	4	16.7	5	1	SUGA_ACHDO
38	3	12.5	5	1	RE31_LITRU
39	2	8.3	4	1	EOSI_HUMAN
40	2	8.3	4	1	YFRI_ATEL
41	2	8.3	4	1	YLM1_YEAST
42	2	8.3	5	1	EI04_LITRU
43	2	8.3	5	1	PSK_DAUCA
44	2	8.3	5	1	UC22_MAIZE
45	2	8.3	5	1	UF01_MOUSE

ALIGNMENTS

RESULT 1
DCMS_PSECH STANDARD; PRT; 4 AA.
AC P19918;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO dehydrogenase subunit S) (CO-DH S) (Fragment).
GN Name-cuts;
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in carboxydohydrogenic bacteria."
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
CC -!- COFACTOR: Binds 2 2Fe-2S clusters (By similarity).
CC -!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small subunit.
DR PIR; P10146; P10146.
KW 2Fe-2S; Direct protein sequencing; Iron; Iron-sulfur; Metal-binding; Oxidoreductase.
FT NON TER 4 4
SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 37.5%; Score 9; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KA 3
Db 3 KA 4

RESULT 2
PFKA_ATEL STANDARD; PRT; 4 AA.
AC P58705;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antho-Kamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;

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RN [1]
RP SEQUENCE.
RX MEDLINE=92028852; PubMed=1691803;
RA Nothern H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-Kaamide), a
RL novel neuropeptide from sea anemones."
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothern H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Kaamide and Antho-Riamide."
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron specific.
DR PIR: J01273; J01273.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 1 1 3-phenyllactic acid.
FT MOD_RES 4 4 Alanine amide.
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match 37.5%; Score 9; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KA 3
DB ||
3 KA 4

RESULT 3
Q08433
ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat."
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL; S38636; AAB19259.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Transferase.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 37.5%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LK 2
DB ||
3 LK 4

RESULT 4
LUXE_VIBFI
ID LUXE_VIBFI STANDARD; PRT; 3 AA.
AC P24272;

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DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
GN Name=luxE;
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072226; PubMed=2254256;
RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
RT site for the lux operon."
RL J. Bacteriol. 172:6797-6802(1990).
CC -!- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It
CC is a component of the fatty acid reductase complex responsible for
CC converting tetradecanoic acid to the aldehyde which serves as
CC substrate in the luciferase-catalyzed reaction.
CC -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
CC an acyl-protein thioester.
CC -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
CC -!- SIMILARITY: Belongs to the luxE family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M62812; -; NOT ANNOTATED_CDS.
KW Ligase; Luminescence.
FT NON_TER 1 1
SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;

Query Match 29.2%; Score 7; DB 1; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LK 2
DB ||
1 LK 2

RESULT 5
ILME_SEPOF
ID ILME_SEPOF STANDARD; PRT; 4 AA.
AC P83568;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Phormone peptide ILME.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=Egg;
RX MEDLINE=20403899; PubMed=10944467; DOI=10.1006/bbrc.2000.3286;
RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
RT "ILME: a waterborne pheromonal peptide released by the eggs of Sepia
RT officinalis."
RL Biochem. Biophys. Res. Commun. 275:217-222(2000).
RN [2]
RP SEQUENCE.
RC TISSUE=Egg;
RX MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;

```

RA Zatylny C., Marvin L., Gagnon J., Henry J.;
 RT "Fertilization in Sepia officinalis: the first mollusk sperm-
 RL attracting peptide.";
 CC -1- BIOCHEM. Biophys. Res. Commun. 296:1186-1193(2002).
 CC -1- FUNCTION: Has myotropic activity targeting the genital tract.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Follicle, fully grown oocyte and egg(EC2).
 CC -1- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
 KW Direct protein sequencing; Phenomone.
 SQ SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;

Query Match 29.2%; Score 7; DB 1; Length 4;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MD 5
 Db 3 ME 4

RESULT 6
 RE11 LITRU STANDARD; PRT; 5 AA.
 ID AC P82070;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Rubellidin 1.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
 CC activity.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -1- MASS SPECTROMETRY: MW=598; METHOD=FAB; RANGE=1-5; NOTE=Ref.1.
 KW Amphibian defense peptide; Direct protein sequencing.
 SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 29.2%; Score 7; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MD 5
 Db 1 VD 2

RESULT 7
 P83073 PRELIMINARY; PRT; 5 AA.
 ID AC P83073;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 88 kDa protein (fragment).
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIMB 11796;

RA Browne N., Dowds B.C.A.;
 RL Submitted (JUL-2001) to Swiss-Prot.
 FT NON TER 5
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 29.2%; Score 7; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LK 2
 Db 1 MK 2

RESULT 8
 ACH1 ACHFU STANDARD; PRT; 4 AA.
 ID AC P35904;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Achatin-I.
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 RC STRAIN=Perussac; TISSUE=Ganglion;
 RX MEDLINE=89273551; PubMed=2597281;
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
 RA Novalles E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 RT fulica Ferussac containing a D-amino acid residue.";
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=Perussac; TISSUE=Heart atrium;
 RX MEDLINE=91264856; PubMed=1675568;
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
 RT "Purification of achatin-I from the atria of the African giant snail,
 RT Achatina fulica, and its possible function.";
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
 RN [3]
 RP CRYSTALLIZATION.
 RX MEDLINE=93014529; PubMed=1399265;
 RA Iwashita T., in Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
 RA Iwashita T., Nomoto K.;
 RT "Crystal structure and molecular conformation of achatin-I (H-Gly-D-
 RT Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid
 RT residue.";
 RL Int. J. Pept. Protein Res. 39:258-264(1992).
 CC -1- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency
 CC and produces a spike broadening of the identified heart excitatory
 CC neuron (PON); also enhances the amplitude and frequency of the
 CC heart beat. Has also an effect on several other muscles.
 DR PIR; A32480; A32480.
 KW D-amino acid; Direct protein sequencing; Hormone.
 FT MOD RES 2 D-Phenylalanine.
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 25.0%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 D 5
 Db 4 D 4

RESULT 9

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FAR3 HIRME
ID FAR3 HIRME STANDARD; PRT; 4 AA.
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRPamide-like neuropeptide YLRP-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rhamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
CC family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 4 4 Phenylalanine amide.
SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 25.0%; Score 6; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LK 2
DB 2 LR 3

RESULT 10
FLRF HIRME STANDARD; PRT; 4 AA.
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FLRFamide.
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421, 27815;
RN [1]
RP SEQUENCE.
RX SPECIES=H. medicinalis;
RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rhamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [2]
RP SEQUENCE.
RX SPECIES=H. trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRPamide-related peptides from the kidney of the snail, Helisoma
trivolvis.";
RL Peptides 15:31-36(1994).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
CC family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 4 4 Phenylalanine amide.
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 25.0%; Score 6; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LK 2
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Db 2 LR 3

RESULT 11
FLRN ANTEL STANDARD; PRT; 4 AA.
ID P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nyantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinscheid R.K., Nothacker H.-P., Staley A.L.;
RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron specific.
CC -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref.1.
DR PIR; A35779; A35779.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 1 1 3-phenyllactic acid.
FT MOD_RES 4 4 Asparagine amide.
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 25.0%; Score 6; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LK 2
DB 2 LR 3

RESULT 12
OCPL OCTMI STANDARD; PRT; 4 AA.
ID OCPL OCTMI STANDARD; PRT; 4 AA.
AC P58648;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cardioactive peptides Ocp-1/Ocp-2.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RX TISSUE=Brain;
RX MEDLINE=203336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
inotropic effects on the heart. Ocp-2 is a 1000 time less active
than Ocp-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
KW D-amino acid; Direct protein sequencing; Hormone.
FT MOD_RES 2 2 D-phenylalanine (in form Ocp-1).
SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;
```

Query Match 25.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 D 5
|
4 D 4

Db

RESULT 13

OCp3_OCTMI STANDARD; PRT; 4 AA.

AC P38649;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Cardioactive peptides Ocp-3/Ocp-4.

OS Octopus minor (Octopus)

OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;

OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.

OX NCBI_TaxID=89766;

RN [1]

RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.

RC TISSUE=Brain;

RX MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;

RA Iwakoshi E., Hisada M., Minakata H.;

RT "Cardioactive peptides isolated from the brain of a Japanese octopus,

RT Octopus minor.";

RL Peptides 21:623-630(2000).

CC -!- FUNCTION: Cardioactive; has both positive chronotropic and

CC inotropic effects on the heart. Ocp-4 is a 1000 time less active

CC than Ocp-3.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.

CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.

CC D-amino acid; Direct protein sequencing; Hormone.

FT MOD_RES 2 D-serine (in form Ocp-4).

SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 25.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 D 5
|
4 D 4

Db

RESULT 14

Q16047 PRELIMINARY; PRT; 4 AA.

AC Q16047;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Interleukin 2 receptor alpha-subunit (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92062171; PubMed=1840490;

RA Mercken L., Moras V., Hemon L., Lionne B., Bousseau A.,

RA Dautry-Varsat A., Collins M., Mayaux J.F.;

RT "An exon 5-deleted mRNA encodes a functional interleukin 2 receptor

RT alpha-subunit.";

RL Biochem. Biophys. Res. Commun. 180:1390-1395(1991).

DR EMBL; S64248; AAB20279.1; -.

DR HSSP; P01112; IPLL.

DR GO; GO:0005525; F:GTP binding; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.

DR

DR InterPro; IPR001806; Ras_trnsfrmng.

DR PRINTS; PR00449; RASTRNSFRMG.

KW Receptor.

FT NON_TER 4 4 525 MW; 69CAB769A0000000 CRC64;

SQ SEQUENCE 4 AA; 525 MW; 69CAB769A0000000 CRC64;

Query Match 25.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 D 5
|
3 D 3

Db

RESULT 15

BIOA_CITFR STANDARD; PRT; 5 AA.

ID BIOA_CITFR

AC P13071;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Adenosylmethionine-8-amino-7-oxononoate aminotransferase

DE (EC 2.6.1.62) (7,8-diamino-peilargonic acid aminotransferase) (DAPA

DE aminotransferase) (Fragment).

GN Name=BIOA;

OS Citrobacter freundii.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Citrobacter.

OX NCBI_TaxID=546;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89006280; PubMed=29711595; DOI=10.1016/0378-1119(88)90397-6;

RA Shiuan D., Campbell A.;

RT "transcriptional regulation and gene arrangement of Escherichia coli,

RT Citrobacter freundii and Salmonella typhimurium biotin operons.";

RL Gene 67:203-211(1988).

CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-

CC oxononoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-

CC diaminononoate.

CC -!- COFACTOR: Pyridoxal phosphate.

CC -!- PATHWAY: Biotin biosynthesis.

CC -!- SUBUNIT: Homodimer.

CC -!- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent

CC aminotransferase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC EMBL; M21922; -; NOT_ANNOTATED_CDS.

DR PIR; I40697; I40697.

DR InterPro; IPR005814; Aminotrans_3.

DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.

KW Aminotransferase; Biotin biosynthesis; Pyridoxal phosphate;

FT NON_TER 5 5 582 MW; 6AAAB1B1A6F00000 CRC64;

SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 25.0%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 D 5
|
4 D 4

Db

Search completed: May 26, 2005, 19:59:10

Job time : 168 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2005, 19:41:29 ; Search time 157 Seconds
(without alignments)
12.317 Million cell updates/sec

Title: US-10-047-945-3

Perfect score: 24

Sequence: 1 LKAMD 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 45841

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	5	2	AAW53842 N-terminu
2	24	100.0	5	7	ABB80224 Synthetic
3	21	87.5	5	2	AAW24922 Vesicular
4	16	66.7	4	7	ABR82923 Tetrapept
5	16	66.7	5	5	AAM49579 Human bet
6	15	62.5	5	3	AAI83346 Peptide m
7	15	62.5	5	4	AAM51285 Anti-Hiv
8	15	62.5	5	4	AAB35188 Human Tra
9	15	62.5	5	7	ADJ82602 Shuffled
10	15	62.5	5	7	ADJ82644
11	15	62.5	5	8	ADM46700 C-termina
12	15	62.5	5	8	ADM46839 Variant a
13	15	62.5	5	8	ADM46841 Variant a
14	15	62.5	5	8	ADQ95007 Synthetic
15	14	58.3	4	2	AAR83230 Integrin-
16	14	58.3	4	2	AAI08030 Biotin de
17	14	58.3	4	3	AAI88365 CCR inhib
18	14	58.3	4	5	AAU74705 Human cel
19	14	58.3	5	2	AAR91816 Mab-425-C
20	14	58.3	5	4	AAM51340 Anti-HIV
21	14	58.3	5	5	ABB46284 Desmoglei
22	14	58.3	5	5	AAO15010 Mutant VH
23	14	58.3	5	7	ADF53341 Adeno-ass
24	13	54.2	4	2	AAW08855 Peptide c
25	13	54.2	4	2	AAW48196 Conantoki

26	13	54.2	4	2	AAW49978
27	13	54.2	4	2	AAI24412
28	13	54.2	4	3	AAI67511
29	13	54.2	4	4	AAI29561
30	13	54.2	4	4	AAI79033
31	13	54.2	4	4	AAI30767
32	13	54.2	4	4	AAI30774
33	13	54.2	4	5	AAM50423
34	13	54.2	4	6	ABB82672
35	13	54.2	4	6	ABG76148
36	13	54.2	4	8	ADJ84013
37	13	54.2	4	8	ADN02852
38	13	54.2	4	8	ADP74548
39	13	54.2	4	8	ADR45776
40	13	54.2	5	2	AAR59983
41	13	54.2	5	2	AAW22550
42	13	54.2	5	3	AAI83312
43	13	54.2	5	5	AAU85930
44	13	54.2	5	7	ADI10462
45	13	54.2	5	7	ABG75419

ALIGNMENTS

RESULT 1
AAW53842
ID AAW53842 standard; peptide; 5 AA.
XX
AC AAW53842;
XX
DT 08-JUL-1998 (first entry)
XX
DE N-terminus of opossum LTNP.
XX
KW LTNP; lethal toxin neutralising factor; opossum; envenomation; therapy;
KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
KW histamine reaction treatment.
XX
OS Didelphis virginiana.
XX
PN US744449-A.
XX
PD 28-APR-1998.
XX
PF 03-JUN-1996; 96US-00657163.
XX
PR 10-MAY-1993; 93US-00058387.
PR 22-SEP-1994; 94US-00310340.
XX
PA (LIPP/) LIPPS B V.
PA (LIPP/) LIPPS F W.
XX
PI Lipps FW, Lipps BV;
XX WPI; 1998-271108/24.
XX
DR Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
PT venom(s) from all major families of poisonous snakes.
XX
PS Claim 5; Col 13; lipp; English.
XX
CC This sequence represents the peptide of the invention. It is a Lethal
CC Toxin Neutralising Factor (LTNP) moiety from a 68 kDa anti-haemorrhagic
CC protein derived from an opossum. The peptide can be used in a method for
CC treating a victim of envenomation from a poisonous snake, preferably a
CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
CC is useful for the treatment of snake bites, sepsis, allergies caused by
CC the environment and treatment of bee or scorpion stings or toxicities
CC caused by plant or bacterial toxins. The peptide can also be used in
CC histamine reaction treatment. The peptide can be used in envenomation
CC treatment for a variety of snakes without prior identification of the

CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins

SQ Sequence 5 AA;
 Query Match 100.0%; Score 24; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMD 5
 Db 1 LKAMD 5

RESULT 2
 ABB80224
 ID ABB80224 standard; peptide; 5 AA.

XX AC ABB80224;
 XX DT 06-NOV-2003 (first entry)
 XX DE Synthetic LTNP, LT-5.
 XX KW Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.

XX OS Synthetic.

XX PN WO2003060471-A2.

XX PD 24-JUL-2003.

XX PF 14-JAN-2003; 2003WO-US001044.

XX PR 14-JAN-2002; 2002US-00047945.

XX PA (LIPP/) LIPPS B V.

XX PA (LIPP/) LIPPS F W.

XX PI Lipps BV, Lipps FW;

XX PS WPI; 2003-636703/60.

XX PT Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

XX PS Disclosure; Page 3; 24pp; English.

XX CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

SQ Sequence 5 AA;
 Query Match 100.0%; Score 24; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMD 5
 Db 1 LKAMD 5

RESULT 3

AAW24922
 ID AAW24922 standard; peptide; 5 AA.

XX AC AAW24922;

XX DT 25-MAR-2003 (revised)

XX DT 17-OCT-1997 (first entry)

XX DE Vesicular stomatitis virus nucleocapsid protein #2.

XX KW Etiological agent; autoimmune disease; systemic lupus erythematosus; SLE;
 KW Ro/SSA; immunoreactive; autoantibody; antigenicity; nucleocapsid;
 KW vesicular stomatitis virus.

XX OS Vesicular stomatitis virus.

XX PN US5637454-A.

XX PD 10-JUN-1997.

XX PF 07-NOV-1994; 94US-00335198.

XX PR 31-JAN-1990; 90US-00472947.

XX PR 31-JAN-1991; 91US-00648205.

XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX PI Harley JB;

XX PS WPI; 1997-319066/29.

XX PT Determination of immunogenic agent in auto-immune disease - by
 PT identifying protein sequences homologous to self-antigen sequences.

XX PS Example 2; Col 17; 36pp; English.

XX CC The invention relates to methods to determine the etiological agent of
 CC autoimmune diseases such as systemic lupus erythematosus (SLE). A common
 CC antigen for SLE and closely related disorders is the 60 kD protein-RNA
 CC particle: Ro/SSA, present in all cells studied to date. Staphylococcus V8
 CC protease digestion of this protein reveals bands of 51, 40, 35, 28 and 13
 CC kD which are strongly immunoreactive with SLE autoantibodies. From the 13
 CC kD band, peptide AAW24911 demonstrated maximal antigenicity against anti-
 CC Ro/SSA autoantibodies. Peptides immunoreactive with SLE autoantibodies
 CC can then be used to screen for other peptides reactive with the
 CC antibodies. An example of such a peptide is the sequence presented here
 CC which is derived from the nucleocapsid protein of the Indiana serotype of
 CC the vesicular stomatitis virus. (Updated on 25-MAR-2003 to correct PF
 CC field.)

SQ Sequence 5 AA;

Query Match 87.5%; Score 21; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5

Db 1 LKAMD 5

AA83346
ID AAY83346 standard; peptide; 5 AA.

AC AAY83346;
XX
DT 16-AUG-2000 (first entry)
XX
DE Peptide motif of SDD1 subtilisin-like serine protease.
XX
XX SDD1; serine protease; subtilisin; transgenic plants; dry weight;
KW stomata; sugar; water; protein; CO_2; H_2O; CO2; H2O; crop protection;
KW feed; foodstuffs.
XX
OS Synthetic.
OS Arabidopsis thaliana.
XX
XX WO200022144-A2.
XX
XX 20-APR-2000.
XX
XX 12-OCT-1999; 99WO-EF007633.
XX
XX 12-OCT-1998; 98EP-00119244.
XX
XX (PLAC) MAX PLANCK GRS FOERDERUNG WISSENSCHAFTEN.
PA (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.
XX
XX Berger D, Altmann T;
XX
XX WPI; 2000-317995/27.
XX
XX Novel recombinant DNA molecules encoding subtilisin-like serine protease,
PT useful for producing transgenic plants with altered stomata, lower water
PT consumption and enhanced disease resistance.
XX
XX Disclosure; Page 6; 101pp; English.
XX
XX Sequences encoding SDD1, a subtilisin-like serine protease, can be used
CC to produce transgenic plants with altered stomata characteristics. These
CC plants exhibit improved freshness, increased dry weight, reduced leaf
CC temperatures, reduced water loss and lower water consumption and for
CC enhancing the sugar and/or protein content of plant leaves, modulating
CC CO_2 uptake into and H_2O release from leaves, for sustained
CC photosynthesis under high intensity conditions or for the improvement of
CC disease resistance of plants. The transgenic plants and cells of such
CC plants are useful in the preparation of feed, food or additives
XX
XX Sequence 5 AA;
SQ
Query Match 62.5%; Score 15; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AMD 5
DB 2 AMD 4
RESULT 7
AAM51285
ID AAM51285 standard; peptide; 5 AA.
XX
XX AAM51285;
XX
XX 03-JAN-2002 (first entry)
XX
XX Anti-HIV peptide with affinity to gp120 number 35.
DE
XX Anti-HIV; vaccine; gp120; human immunodeficiency virus.
KW
XX Synthetic.
OS
XX JP2001192399-A.
PN
XX 17-JUL-2001.
PD
XX

PF 11-JAN-2000; 2000JP-00006182.
XX
PR 11-JAN-2000; 2000JP-00006182.
XX
PA (FUJI/) FUJII T.
XX
XX WPI; 2001-605354/69.
XX
XX Novel peptides with affinity to gp 120, useful for treatment of HIV.
PT
XX
XX Example 2; Page 8; 21pp; Japanese.
XX
XX The invention relates to peptides (AAM51251-AAM51381) with a higher
CC affinity to gp120, part of the outer shell of HIV, than known peptides.
CC Peptides with affinity to gp120 shown by formula (H-)-Al-A2-A3-A4-A5-R.
CC (1), Al'-A2-A3-A4-A5-R (2) or H-Al-A2-A3-A4-A5'-R (3); (H-)-Al-a2-a3-a4-
CC a5(-R) (4), Al'-a2-a3-a4-a5-R (5) or H-Al-a2-a3-a4-a5'-R (6). Al = Asp,
CC Lys, Val, Glu, Gly, Asn or Tyr residue; A2 = Val, Asp, Trp, Lys, Phe,
CC Ile, Leu or Tyr residue; A3 = Lys, Val, Arg, Ala or Trp residue; A4
CC = Ala, Trp or Gly residue; A5 = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met,
CC Asn, Gln, His, Lys, Arg, Phe, Trp, Pro or Tyr residue; R = OH derived
CC from carboxyl group or NH_2 derived form acid amide group; Al' = Asp,
CC Lys, Val, Glu, Gly, Asn or Tyr residue, or a polypeptide residue having
CC optional amino acids at N-terminal; A5' = Gly, Ala, Val, Leu, Ile, Ser,
CC Thr, Met, Asn, Gln, His, Lys, Arg, Phe, Trp, Pro or Tyr residue, or a
CC polypeptide residue having optional amino acids at C-terminal; Al = Tyr,
CC Arg, Phe, Gly, Trp, His or Asp residue; a2 = Arg, Tyr, Trp, Ala, Val,
CC Gln, His or Lys residue; a3 = Lys, Tyr, Arg, Glu, Met or Trp residue; a4
CC = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asp, Gln, His, Lys, Arg, Phe or
CC Trp residue; a5 = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
CC Lys, Arg, Phe, Tyr or Trp residue; Al' = Tyr, Arg, Phe, Gly, Trp, His or
CC Asp residue, or a polypeptide residue having optional amino acids at N-
CC terminal; and a5' = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln,
CC His, Lys, Arg, Phe, Tyr or Trp, or a polypeptide residue having optional
CC amino acids at C-terminal. The peptides are useful in the treatment of
CC HIV and in the preparation of a HIV vaccine
XX
XX Sequence 5 AA;
SQ
Query Match 62.5%; Score 15; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAM 4
DB 2 VKAM 5
RESULT 8
AAB35188
ID AAB35188 standard; peptide; 5 AA.
XX
XX AAB35188;
AC
XX
XX 09-APR-2001 (first entry)
DT
XX
XX Human Traf 6 aptamer clone peptide SEQ ID NO: 39.
DE
XX
XX Human; protein degradation; siah-mediated degradation protein; SMDP;
KW SCF-complex protein; SCP; siah-1alpha; siah-1 interacting protein; SIP;
KW Skp1-associated F-box protein; SAF-1; SAF-2; SAD; cancer; cell division;
KW Skp1-associated destruction-box protein; inflammatory disease.
XX
XX Homo sapiens.
OS
XX WO200077207-A2.
PN
XX 21-DEC-2000.
PD
XX 09-JUN-2000; 2000WO-US015873.
PF
XX 11-JUN-1999; 99US-00330517.
PR
XX

CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell
 CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
 CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
 CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
 CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
 CC muscle or bone cell. The peptides are also useful for treating fibrotic
 CC disorders, myeloproliferative diseases, and blood vessel proliferative
 CC (angiogenic) disorders. This sequence represents a shuffled P3 peptide.
 XX
 SQ Sequence 5 AA;

Query Match

Best Local Similarity 62.5%; Score 15; DB 7; Length 5;

Mismatches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAM 4
 Db |||
 1 LKSM 4

RESULT 11

ADM46700

ID ADM46700 standard; peptide; 5 AA.

AC ADM46700;

XX 03-JUN-2004 (first entry)

DE C-terminal CDRH3 peptide.

XX variant; CDRH3; CDR; complementarity determining region; antibody;

XX domain; phage; library; antigen.

XX Unidentified.

XX WO2003102157-A2.

XX 11-DEC-2003.

XX 03-JUN-2003; 2003WO-US017545.

XX 03-JUN-2002; 2002US-0385338P.

XX 16-APR-2003; 2003US-0463656P.

XX (GETH) GENENTECH INC.

XX Fuh GG, Sidhu SS;

XX WPI; 2004-043102/04.

XX New polypeptide useful for selecting antigen for antigen binding variable
 PT domain that binds to target antigen.

XX Disclosure; SEQ ID NO 4; 205pp; English.

XX The invention relates to a novel polypeptide comprising a variant CDRH3
 CC antibody variable domain. The invention further provides an antibody
 CC phage library. The variant CDRH3 polypeptide is useful for selecting an
 CC antigen for an antigen binding variable domain that binds to a target.
 CC The phage library is useful for selecting a polypeptide that binds to a
 CC target antigen from the library of polypeptides and isolating high
 CC affinity binders to a target antigen from the library of replicable
 CC expression vectors. This sequence represents a variable antibody domain
 CC related polypeptide of the invention.
 XX
 SQ Sequence 5 AA;

Query Match

Best Local Similarity 62.5%; Score 15; DB 8; Length 5;

Mismatches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AMD 5
 |||

Db 2 AMD 4

RESULT 12

ADM46839

ID ADM46839 standard; peptide; 5 AA.

XX ADM46839;

XX 03-JUN-2004 (first entry)

XX Variant antibody variable domain peptide, C-terminal of CDRH3.

XX variant; CDRH3; CDR; complementarity determining region; antibody;

XX domain; phage; library; antigen.

XX Unidentified.

XX WO2003102157-A2.

XX 11-DEC-2003.

XX 03-JUN-2003; 2003WO-US017545.

XX 03-JUN-2002; 2002US-0385338P.

XX 16-APR-2003; 2003US-0463656P.

XX (GETH) GENENTECH INC.

XX Fuh GG, Sidhu SS;

XX WPI; 2004-043102/04.

XX New polypeptide useful for selecting antigen for antigen binding variable
 PT domain that binds to target antigen.

XX Disclosure; SEQ ID NO 163; 205pp; English.

XX The invention relates to a novel polypeptide comprising a variant CDRH3
 CC antibody variable domain. The invention further provides an antibody
 CC phage library. The variant CDRH3 polypeptide is useful for selecting an
 CC antigen for an antigen binding variable domain that binds to a target.
 CC The phage library is useful for selecting a polypeptide that binds to a
 CC target antigen from the library of polypeptides and isolating high
 CC affinity binders to a target antigen from the library of replicable
 CC expression vectors. This sequence represents a variable antibody domain
 CC related polypeptide of the invention.
 XX
 SQ Sequence 5 AA;

Query Match

Best Local Similarity 62.5%; Score 15; DB 8; Length 5;

Mismatches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AMD 5
 |||
 Db 2 AMD 4

RESULT 13

ADM46841

ID ADM46841 standard; peptide; 5 AA.

XX ADM46841;

XX 03-JUN-2004 (first entry)

XX Variant antibody variable domain, CDRH3 C-terminal peptide.

XX variant; CDRH3; CDR; complementarity determining region; antibody;

XX domain; phage; library; antigen.

XX Unidentified.

XX WO2003102157-A2.
 XX 11-DEC-2003.
 XX 03-JUN-2003; 2003WO-US017545.
 XX 03-JUN-2002; 2002US-0385338P.
 XX 16-APR-2003; 2003US-0463656P.
 XX (GETH) GENENTECH INC.
 XX Fuh GG, Sidhu SS;
 XX WPI; 2004-043102/04.
 XX New polypeptide useful for selecting antigen for antigen binding variable
 PT domain that binds to target antigen.
 XX Disclosure; Page 7; 205pp; English.
 XX The invention relates to a novel polypeptide comprising a variant CDRH3
 CC antibody variable domain. The invention further provides an antibody
 CC phage library. The variant CDRH3 polypeptide is useful for selecting an
 CC antigen for an antigen binding variable domain that binds to a target.
 CC The phage library is useful for selecting a polypeptide that binds to a
 CC target antigen from the library of polypeptides and isolating high
 CC affinity binders to a target antigen from the library of replicable
 CC expression vectors. This sequence represents a variable antibody domain
 CC related polypeptide of the invention.
 XX Sequence 5 AA;
 SQ

Query Match 62.5%; Score 15; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AMD 5
 Db 2 AMD 4

RESULT 14
 ADQ95007
 ID ADQ95007 standard; peptide; 5 AA.
 XX AC ADQ95007;
 XX DT 21-OCT-2004 (first entry)
 XX DE Synthetic phage antibody library-related 4D5 antibody peptide SeqID4.
 XX KW complementarity determining region; heavy chain 3; CDRH3; CDRH3 scaffold;
 KW synthetic antibody phage library; binding affinity; structural stability;
 KW immunoglobulin.
 XX OS Synthetic.
 XX OS Unidentified.
 XX WO2004065416-A2.
 XX 05-AUG-2004.
 XX 16-JAN-2004; 2004WO-US001097.
 XX 16-JAN-2003; 2003US-0441059P.
 XX 18-JUL-2003; 2003US-0488610P.
 XX 08-OCT-2003; 2003US-0510314P.
 XX (GETH) GENENTECH INC.
 XX Bond CJ;
 XX

DR WPI; 2004-580713/56.
 XX New polypeptide comprising variant complementarity determining region of
 PT heavy chain 3 having structural amino acid positions, and non-structural
 PT positions having variant amino acid, useful for identifying antigen
 PT binding polypeptides.
 XX Disclosure; SEQ ID NO 4; 238pp; English.
 XX This invention relates to a novel polypeptide comprising a variant
 CC complementarity determining region of heavy chain 3 (CDRH3) region
 CC comprising at least one structural amino acid position, and at least one
 CC non-structural position having a variant amino acid. The invention is
 CC useful for designing a CDRH3 scaffold and the polypeptides are useful as
 CC a source for identifying novel antigen binding polypeptides and antibody
 CC variable domains that can be used therapeutically or as reagents. A
 CC synthetic antibody phage library of these polypeptides is useful for
 CC screening synthetic antibody or antigen binding polypeptide with
 CC desirable activity such as binding affinities and structural stability.
 CC The library is also useful as resource for identifying immunoglobulin
 CC polypeptide sequences that are capable of interacting with any of a wide
 CC variety of target molecules. The invention provides high throughput,
 CC efficient and automatable systems for screening antigen binding molecules
 CC of interest. The present sequence is that of a peptide which is related
 CC to the novel polypeptide of the invention.
 XX Sequence 5 AA;
 SQ

Query Match 62.5%; Score 15; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AMD 5
 Db 2 AMD 4

RESULT 15
 AAR83230
 ID AAR83230 standard; peptide; 4 AA.
 XX AC AAR83230;
 XX DT 26-JAN-1996 (first entry)
 XX DE Integrin-inhibiting peptide fragment.
 XX KW platelet integrin; gp IIB/IIIA; thrombosis; infarction; inflammation;
 KW coronary heart disease; arteriosclerosis; atherosclerosis; stroke;
 KW angina pectoris; tumour; osteoporosis; angiogenesis; reatenosis;
 KW wound healing; ligand; integrin; affinity chromatography.
 XX OS Synthetic.
 XX DB4336758-A1.
 XX 04-MAY-1995.
 XX 28-OCT-1993; 93DE-04336758.
 XX 28-OCT-1993; 93DE-04336758.
 XX (MERE) MERCK PATENT GMBH.
 XX Jonczyk A, Felding-Habermann B, Diefenbach B, Rippmann F;
 XX WPI; 1995-171142/23.
 XX New cysteine contg. peptide derivs. which inhibit platelet integrin - are
 PT useful for treating or preventing circulatory disease, thrombosis, etc.,
 PT also for affinity purification. of integrins.
 XX Claim 1; Page 15; 16pp; German.
 XX

XX The invention relates to new linear peptides of formula X-A-Cys(R1)-B-Z
CC in which X is H or Ac; A is absent or is Asp or a specified polypeptide;
CC B is absent or a specified amino acid or polypeptide; A and B cannot both
CC be absent; and Z is OH or an ester or amide group. The peptides inhibit
CC binding of the platelet integrin gpIIb/IIIa to its natural ligands and so
CC are useful for preventing circulatory diseases, thrombosis, cardiac
CC infarction, inflammation, coronary heart disease, arteriosclerosis,
CC atherosclerosis, stroke, angina pectoris, tumour, osteoporosis,
CC angiogenesis and restenosis. They are also useful for promoting healing
CC of wounds and as ligands for purification of integrins by affinity
CC chromatography. The present sequence is a specific example of the
CC polypeptide fragment A
XX
SQ Sequence 4 AA;

Query Match 58.3%; Score 14; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMD 5
Db |||
1 KAAD 4

Search completed: May 26, 2005, 19:56:21
Job time : 165 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2005, 19:59:17 ; Search time 134 Seconds
(without alignments)
12.872 Million cell updates/sec

Title: US-10-047-945-3

Perfect score: 24

Sequence: 1 LKAMD 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 23607

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	5	14	US-10-047-945-3
2	15	62.5	5	16	US-10-679-246-39
3	15	62.5	5	17	US-10-783-311-107
4	15	62.5	5	17	US-10-759-731A-4
5	14	58.3	4	9	US-09-016-750C-17
6	14	58.3	4	9	US-09-016-869B-17
7	14	58.3	4	10	US-09-947-206-17
8	14	58.3	5	9	US-09-817-661-26
9	14	58.3	5	17	US-10-099-442-2
10	14	58.3	5	17	US-10-911-065-2
11	13	54.2	4	13	US-10-115-704-9
12	13	54.2	4	14	US-10-357-467-33
13	13	54.2	4	17	US-10-808-187-88
					Sequence 3, Appl
					Sequence 39, Appl
					Sequence 107, Appl
					Sequence 4, Appl
					Sequence 17, Appl
					Sequence 17, Appl
					Sequence 26, Appl
					Sequence 2, Appl
					Sequence 2, Appl
					Sequence 9, Appl
					Sequence 33, Appl
					Sequence 88, Appl

14	13	54.2	5	15	US-10-156-214A-93	Sequence 93, Appl
15	13	54.2	5	15	US-10-417-476-59	Sequence 59, Appl
16	12	50.0	4	9	US-09-782-980-110	Sequence 110, Appl
17	12	50.0	4	9	US-09-915-306-5	Sequence 5, Appl
18	12	50.0	4	9	US-09-915-306-6	Sequence 6, Appl
19	12	50.0	4	9	US-09-915-306-7	Sequence 7, Appl
20	12	50.0	4	9	US-09-915-306-8	Sequence 8, Appl
21	12	50.0	4	9	US-09-915-374-5	Sequence 5, Appl
22	12	50.0	4	9	US-09-915-374-6	Sequence 6, Appl
23	12	50.0	4	9	US-09-915-374-7	Sequence 7, Appl
24	12	50.0	4	9	US-09-915-374-8	Sequence 8, Appl
25	12	50.0	4	14	US-10-214-932-114	Sequence 114, Appl
26	12	50.0	4	15	US-10-435-751-89	Sequence 89, Appl
27	12	50.0	4	16	US-10-806-018-110	Sequence 110, Appl
28	12	50.0	5	8	US-08-424-550B-404	Sequence 404, Appl
29	12	50.0	5	9	US-09-915-306-20	Sequence 20, Appl
30	12	50.0	5	9	US-09-915-374-20	Sequence 20, Appl
31	12	50.0	5	10	US-09-788-006-74	Sequence 74, Appl
32	12	50.0	5	10	US-09-788-006-75	Sequence 75, Appl
33	12	50.0	5	14	US-10-006-869-437	Sequence 437, Appl
34	12	50.0	5	14	US-10-006-869-3019	Sequence 3019, Appl
35	12	50.0	5	15	US-10-395-032-437	Sequence 437, Appl
36	12	50.0	5	15	US-10-395-032-3019	Sequence 3019, Appl
37	12	50.0	5	15	US-10-436-549-22	Sequence 22, Appl
38	12	50.0	5	15	US-10-436-549-134	Sequence 134, Appl
39	12	50.0	5	15	US-10-374-466-42	Sequence 42, Appl
40	12	50.0	5	16	US-10-712-425-22	Sequence 22, Appl
41	12	50.0	5	16	US-10-712-425-134	Sequence 134, Appl
42	12	50.0	5	17	US-10-783-311-251	Sequence 251, Appl
43	12	50.0	5	17	US-10-808-187-467	Sequence 467, Appl
44	12	50.0	5	17	US-10-938-249-115	Sequence 115, Appl
45	12	50.0	5	17	US-10-773-032-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-10-047-945-3
; Sequence 3, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-3

Query Match 100.0%; Score 24; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. NO. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5

Db 1 LKAMD 5

RESULT 2
US-10-679-246-39
; Sequence 39, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Matsuzawa, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: In Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: 66821-235
; CURRENT APPLICATION NUMBER: US/10/679,246
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-679-246-39

Query Match 62.5%; Score 15; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AMD 5
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DB 3 AMD 5

RESULT 3
US-10-783-311-107
; Sequence 107, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-783-311-107

Query Match 62.5%; Score 15; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AMD 5
|||
DB 3 AMD 5

RESULT 4
US-10-759-731A-4
; Sequence 4, Application US/10759731A
; Publication No. US20050079574A1
; GENERAL INFORMATION:
; APPLICANT: Bond, Christopher J.
; TITLE OF INVENTION: SYNTHETIC ANTIBODY PHAGE LIBRARIES
; FILE REFERENCE: 11669-136USU1
; CURRENT APPLICATION NUMBER: US/10/759,731A
; CURRENT FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: US 60/441,059
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/488,610
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/510,314
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C-terminal of CDRH3 of 4DS
US-10-759-731A-4

Query Match 62.5%; Score 15; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AMD 5
|||
DB 2 AMD 4

RESULT 5
US-09-016-750C-17
; Sequence 17, Application US/09016750C
; Patent No. US2002025305A1
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES
; TITLE OF INVENTION: RELATED THERETO
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HONG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,750C
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/893,274
; FILING DATE: 15-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/09945
 ; FILING DATE: 18-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REGISTRATION NUMBER: 36,709
 ; REFERENCE/DOCKET NUMBER: MIV-071.13
 ; TELEPHONE: 617-832-1000
 ; TELEFAX: 617-832-7000
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-016-750C-17

Query Match 58.3%; Score 14; DB 9; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.3e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMD 5
 Db 1 KARD 4

RESULT 6
 US-09-016-869B-17
 ; Sequence 17, Application US/09016869B
 ; Patent No. US2002082392A1

; GENERAL INFORMATION:
 ; APPLICANT: Beach, David H.
 ; APPLICANT: Demetrick, Douglas J.
 ; APPLICANT: Serrano, Manuel
 ; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
 ; TITLE OF INVENTION: Uses Related Thereto
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ropes & Gray
 ; STREET: One International Place
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Wordpad
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016.869B
 ; FILING DATE: 30-JAN-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/893,274
 ; FILING DATE: 15-JUL-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/306,511
 ; FILING DATE: 14-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/248,812
 ; FILING DATE: 25-MAY-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/227,371
 ; FILING DATE: 14-APR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/154,915
 ; FILING DATE: 18-NOV-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/991,997
 ; FILING DATE: 17-DEC-1992

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REGISTRATION NUMBER: 36,709
 ; REFERENCE/DOCKET NUMBER: GPCI-P10-071
 ; TELEPHONE: 617 951-7739
 ; TELEFAX: 617 951-7050
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-016-869B-17

Query Match 58.3%; Score 14; DB 9; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.3e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMD 5
 Db 1 KARD 4

RESULT 7

US-09-947-206-17
 ; Sequence 17, Application US/09947206
 ; Publication No. US20030100489A1

; GENERAL INFORMATION:
 ; APPLICANT: Beach, David H.
 ; APPLICANT: Demetrick, Douglas J.
 ; APPLICANT: Serrano, Manuel
 ; APPLICANT: Hannon, Gregory J.

; TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES
 ; TITLE OF INVENTION: RELATED THERETO
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109-2170

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/947,206
 ; FILING DATE: 04-Sep-2001
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/016,750
 ; FILING DATE: 1998-01-03
 ; APPLICATION NUMBER: US 08/306,511
 ; FILING DATE: 14-SEP-1994
 ; APPLICATION NUMBER: US 08/248,812
 ; FILING DATE: 25-MAY-1994
 ; APPLICATION NUMBER: US 08/227,371
 ; FILING DATE: 14-APR-1994
 ; APPLICATION NUMBER: US 08/154,915
 ; FILING DATE: 18-NOV-1993
 ; APPLICATION NUMBER: US 07/991,997
 ; FILING DATE: 17-DEC-1992
 ; APPLICATION NUMBER: US 07/963,308
 ; FILING DATE: 16-OCT-1992
 ; APPLICATION NUMBER: PCT/US93/09945
 ; FILING DATE: 18-OCT-1993

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REGISTRATION NUMBER: 36,709
 ; REFERENCE/DOCKET NUMBER: MIV-071.13

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-947-206-17

Query Match 58.3%; Score 14; DB 10; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMD 5
DB 1 KARD 4

RESULT 8

US-09-817-661-26
; Sequence 26, Application US/09817661
; Patent No. US20020076692A1
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane
; APPLICANT: Holet, Thor
; TITLE OF INVENTION: Improvements to ribosome display
; FILE REFERENCE: 84633
; CURRENT APPLICATION NUMBER: US/09/817,661
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/193,802
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutagenized
US-09-817-661-26

Query Match 58.3%; Score 14; DB 9; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KAMD 5
DB 1 RSMO 4

RESULT 9

US-10-099-442-2
; Sequence 2, Application US/10099442
; Publication No. US20030129604A1
; GENERAL INFORMATION:
; APPLICANT: Lockhart, David J.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Langer-Safer, Pennina
; TITLE OF INVENTION: Identification of Molecular Sequence Signatures and Methods Invol
; FILE REFERENCE: 3016.2A
; CURRENT APPLICATION NUMBER: US/10/099,442
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/321,481
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic sequence.
US-10-099-442-2

Query Match 58.3%; Score 14; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KAM 4
DB 3 KAM 5

RESULT 10

US-10-911-065-2
; Sequence 2, Application US/10911065
; Publication No. US20050069927A1
; GENERAL INFORMATION:
; APPLICANT: Lockhart, David J.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Langer-Safer, Pennina
; TITLE OF INVENTION: Identification of Molecular Sequence Signatures and Methods Invol
; FILE REFERENCE: 3016.2A
; CURRENT APPLICATION NUMBER: US/10/911,065
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US/10/099,442
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/321,481
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic sequence.
US-10-911-065-2

Query Match 58.3%; Score 14; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KAM 4
DB 3 KAM 5

RESULT 11

US-10-115-704-9
; Sequence 9, Application US/10115704
; Publication No. US20020192780A1
; GENERAL INFORMATION:
; APPLICANT: SOHN, JOON HONG
; APPLICANT: KIM, SOO YOUNG
; TITLE OF INVENTION: NOVEL ANTI-INFLAMMATORY PEPTIDES
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/115,704
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: KR10-2001-21598
; PRIOR FILING DATE: 2001-04-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Kopatent In 1.71
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC

US-10-115-704-9

Query Match 54.2%; Score 13; DB 13; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMD 5
| : |
Db 1 KVLVD 4

RESULT 12

US-10-357-467-33
; Sequence 33, Application US/10357467
; Publication No. US20030194729A1
; GENERAL INFORMATION:

APPLICANT: Abogadie, Fe C.
Cruz, Lourdes J.
Olivera, Baldomero M.
Walker, Craig
Collidge, Clark
Hillyard, David R.
Jimenez, Elsie

TITLE OF INVENTION: Conantokins
NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Earnat & Manbeck, p.c.
STREET: 1425 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20005

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/357,467

FILING DATE: 04-Feb-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/142,080

FILING DATE: 15-MAY-2000

APPLICATION NUMBER: WO US97/12618

FILING DATE: 21-JUL-1997

APPLICATION NUMBER: US 08/684,742

FILING DATE: 22-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 2314-256.A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-783-6040

TELEFAX: 202-783-6031

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: C-terminal

SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-10-357-467-33

Query Match 54.2%; Score 13; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKA 3
| : |
Db 2 LKA 4

RESULT 13

US-10-808-187-88
; Sequence 88, Application US/10808187

; Publication No. US2005009009A1

; GENERAL INFORMATION:

APPLICANT: PEIRIS, JOSEPH S. M.

APPLICANT: YUEN, KWOK YUNG

APPLICANT: POON, LIT MAN

APPLICANT: GUAN, YI

APPLICANT: CHAN, KWOK HUNG

APPLICANT: NICHOLLS, JOHN

TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE

FILE REFERENCE: V9661.0078

CURRENT APPLICATION NUMBER: US/10/808,187

CURRENT FILING DATE: 2004-03-24

PRIOR APPLICATION NUMBER: 60/457,031

PRIOR FILING DATE: 2003-03-24

PRIOR APPLICATION NUMBER: 60/457,730

PRIOR FILING DATE: 2003-03-26

PRIOR APPLICATION NUMBER: 60/459,931

PRIOR FILING DATE: 2003-04-02

PRIOR APPLICATION NUMBER: 60/460,357

PRIOR FILING DATE: 2003-04-03

PRIOR APPLICATION NUMBER: 60/461,265

PRIOR FILING DATE: 2003-04-08

PRIOR APPLICATION NUMBER: 60/462,805

PRIOR FILING DATE: 2003-04-14

PRIOR APPLICATION NUMBER: 60/468,139

PRIOR FILING DATE: 2003-05-05

PRIOR APPLICATION NUMBER: 60/464,886

PRIOR FILING DATE: 2003-04-23

PRIOR APPLICATION NUMBER: 60/471,200

PRIOR FILING DATE: 2003-05-16

NUMBER OF SEQ ID NOS: 2476

SOFTWARE: Patent in ver. 3.2

SEQ ID NO 88

LENGTH: 4

TYPE: PRT

ORGANISM: Human severe acute respiratory system virus

US-10-808-187-88

Query Match 54.2%; Score 13; DB 17; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.3e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKA 3
| : |
Db 1 LKA 3

RESULT 14

US-10-156-214A-93

; Sequence 93, Application US/10156214A

; Publication No. US20040001801A1

; GENERAL INFORMATION:

APPLICANT: Edwin L. Madison

APPLICANT: Joseph Edward Sample

APPLICANT: George P. Vlasuk

APPLICANT: Scott Jeffrey Kemp

APPLICANT: Mallareddy Komandla

APPLICANT: Daniel Vanna Slev

TITLE OF INVENTION: Conjugates Activated By Cell Surface Proteases and Therapeutic Us

FILE REFERENCE: 24745-1611

CURRENT APPLICATION NUMBER: US/10/156,214A

CURRENT FILING DATE: 2002-05-23

NUMBER OF SEQ ID NOS: 611

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 93

LENGTH: 5

TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Conjugate
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa is H-D-Val
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 5
; OTHER INFORMATION: Alanine-therapeutic agent
US-10-156-214A-93

Query Match 54.2%; Score 13; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKA 3
Db 2 LKA 4

RESULT 15
US-10-417-476-59
; Sequence 59, Application US/10417476
; Publication No. US20040002102A1
; GENERAL INFORMATION:
; APPLICANT: Litman, Gary W.
; APPLICANT: Hawke, No. US20040002102A11 A.
; APPLICANT: Yoder, Jeffrey A.
; APPLICANT: Eason, Donna D.
; TITLE OF INVENTION: B1VM (Basic, Immunoglobulin-Like Variable Motif-Containing) Gene,
; FILE REFERENCE: USP-103X
; CURRENT APPLICATION NUMBER: US/10/417,476
; CURRENT FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B1VM N-terminus region of homology
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa = Val or Cys
US-10-417-476-59

Query Match 54.2%; Score 13; DB 15; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMD 5
Db 2 KXLD 5

Search completed: May 26, 2005, 20:12:33
Job time : 172 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 19:50:26 ; Search time 40 Seconds
(without alignments)
9.331 Million cell updates/sec

Title: US-10-047-945-3

Perfect score: 24

Sequence: 1 LKAMD 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 27945

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	5	1	US-08-657-163A-3
2	21	87.5	5	1	US-08-335-198-20
3	15	62.5	5	2	US-08-350-260A-413
4	15	62.5	5	4	US-09-104-337A-413
5	15	62.5	5	4	US-09-591-594-39
6	14	58.3	4	1	US-08-329-820-4
7	14	58.3	4	1	US-08-329-820-88
8	14	58.3	4	3	US-08-581-918A-17
9	14	58.3	4	3	US-08-346-147B-17
10	14	58.3	4	3	US-08-497-214D-17
11	14	58.3	4	4	US-09-016-750C-17
12	14	58.3	5	2	US-08-528-523-2
13	14	58.3	5	3	US-08-933-219B-2
14	14	58.3	5	3	US-09-321-481-2
15	14	58.3	5	4	US-09-535-852-1028
16	13	54.2	4	3	US-08-859-242-34
17	13	54.2	4	3	US-08-859-242-41
18	13	54.2	4	3	US-09-142-078-33
19	13	54.2	4	3	US-09-357-141-33
20	13	54.2	4	3	US-09-533-889-33
21	13	54.2	5	1	US-09-142-080-33
22	13	54.2	5	1	US-08-477-727A-16
23	13	54.2	5	1	US-08-477-727A-28
24	13	54.2	5	1	US-08-477-727A-41
25	13	54.2	5	4	US-09-608-892-55
26	13	54.2	5	5	PCT-US93-12679-40
27	12	50.0	4	1	US-08-208-108-14

28 12 50.0 4 3 US-09-162-366C-5 Sequence 5, Appli
29 12 50.0 4 3 US-09-162-366C-6 Sequence 6, Appli
30 12 50.0 4 3 US-09-162-366C-7 Sequence 7, Appli
31 12 50.0 4 3 US-09-162-366C-8 Sequence 8, Appli
32 12 50.0 4 4 US-08-657-759-36 Sequence 36, Appli
33 12 50.0 4 4 US-09-535-852-180 Sequence 180, App
34 12 50.0 4 4 US-09-915-374-5 Sequence 5, Appli
35 12 50.0 4 4 US-09-915-374-6 Sequence 6, Appli
36 12 50.0 4 4 US-09-915-374-7 Sequence 7, Appli
37 12 50.0 4 4 US-09-915-374-8 Sequence 8, Appli
38 12 50.0 4 4 US-09-915-306-5 Sequence 5, Appli
39 12 50.0 4 4 US-09-915-306-6 Sequence 6, Appli
40 12 50.0 4 4 US-09-915-306-7 Sequence 7, Appli
41 12 50.0 4 4 US-09-915-306-8 Sequence 8, Appli
42 12 50.0 5 3 US-08-860-248C-39 Sequence 39, Appli
43 12 50.0 5 3 US-09-162-366C-20 Sequence 20, Appli
44 12 50.0 5 3 US-09-187-859-437 Sequence 437, App
45 12 50.0 5 3 US-09-187-859-3019 Sequence 3019, Ap

ALIGNMENTS

RESULT 1
US-08-657-163A-3
; Sequence 3, Application US/08657163A
; Patent No. 5744449
; GENERAL INFORMATION:
; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
; TITLE OF INVENTION: SYNTHETIC LIPIDS AND THEIR
; TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BINIE V. LIPPS
; STREET: 4509 MIMOSA DR.
; CITY: BELLAIRE
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
; SOFTWARE: MS WORD 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,163A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,340
; FILING DATE: 22 SEPTEMBER 1994
; CLASSIFICATION: 514
; APPLICATION NUMBER: 08/058,387
; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN R. CASPERSON
; REGISTRATION NUMBER: 28,198
; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-482-2961
; TELEFAX: 713-663-7290
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 3
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: N

ORIGINAL SOURCE: SYNTHETIC
US-08-657-163A-3

Query Match 100.0%; Score 24; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
|||
DB 1 LKAMD 5

RESULT 2

US-08-335-198-20
; Sequence 20, Application US/08335198
; Patent No. 5637454
; GENERAL INFORMATION:
; APPLICANT: Harlev, John B.
; TITLE OF INVENTION: Assays and Treatments for Autoimmune
; DISEASES
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street, Ste. 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30309-4539
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335.198
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648205
; FILING DATE: 01-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF 114CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 815-8508
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-335-198-20

Query Match 87.5%; Score 21; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
|||
DB 1 LKAMD 5

RESULT 3

US-08-350-260A-413
; Sequence 413, Application US/08350260A

Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350.260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 413:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-413

Query Match 62.5%; Score 15; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKAMD 5
|||
DB 1 LKAMD 4

RESULT 4
US-09-104-337A-413
; Sequence 413, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; ADDRESS: Marshall, Gerstein & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 413:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 413:
US-09-104-337A-413
Query Match 62.5%; Score 15; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 KAMD 5
Db 1 KRMD 4
RESULT 5
US-09-591-694-39
; Sequence 39, Application US/09591694

; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; CURRENT FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330,517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-591-694-39
Query Match 62.5%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 AMD 5
Db 3 AMD 5
RESULT 6
US-08-329-820-4
; Sequence 4, Application US/08329820
; Patent No. 5747457
; GENERAL INFORMATION:
; APPLICANT: JONCZYK, ALFRED
; APPLICANT: FELDING-HABERMANN, BRUNHILDE
; APPLICANT: DIEPENBACH, BEATE
; APPLICANT: RIPPWANN, FRIEDRICH
; TITLE OF INVENTION: Linear Adhesion Inhibitors
; NUMBER OF SEQUENCES: 228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,820
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4336758.5
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1635
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-329-820-4
Query Match 58.3%; Score 14; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMD 5
|||
Db 1 KAAD 4

RESULT 7

US-08-329-820-88
; Sequence 88, Application US/08329820
; Patent No. 574757
; GENERAL INFORMATION:
; APPLICANT: JONCZYK, ALFRED
; APPLICANT: FELDING-HABERMANN, BRUNHILDE
; APPLICANT: DIEFENBACH, BEATE
; APPLICANT: RIPPWANN, FRIEDRICH
; TITLE OF INVENTION: Linear Adhesion Inhibitors
; NUMBER OF SEQUENCES: 228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,820
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4336758.5
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1635
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "Lys(BOC)"
; OTHER INFORMATION: /note= "N-terminal: Fmoc"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Asp(OBut)"
US-08-329-820-88

Query Match 58.3%; Score 14; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMD 5
|||
Db 1 KAAD 4

RESULT 8

US-08-581-918A-17
; Sequence 17, Application US/08581918A
; Patent No. 6043030
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.

; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordpad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/581,918A
; FILING DATE: 02-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/497,214
; FILING DATE: 30-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-581-918A-17

Query Match 58.3%; Score 14; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMD 5
|||
Db 1 KARD 4

RESULT 9

US-08-346-147B-17
; Sequence 17, Application US/08346147B
; Patent No. 6211334
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.

APPLICANT: Demetrick, Douglas J.
 APPLICANT: Serrano, Manuel
 APPLICANT: Hannon, Gregory J.
 TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
 TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley, Hoag & Eliot
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordpad
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/346,147B
 FILING DATE: 29-NOV-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/306,511
 FILING DATE: 14-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/248,812
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/227,371
 FILING DATE: 14-APR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/154,915
 FILING DATE: 18-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/991,997
 FILING DATE: 17-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: MIV-071.04
 TELEPHONE: (617) 832-7000
 TELEFAX: (617) 832-7000
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-346-147B-17
 Query Match 58.3%; Score 14; DB 3; Length 4;
 Best Local Similarity 75.0%; Pred. No. 4.1e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 KAMD 5
 Db 1 KARD 4
 RESULT 10
 US-08-497-214D-17
 Sequence 17, Application US/08497214D
 Patent No. 6331390
 GENERAL INFORMATION:
 APPLICANT: Beach, David H.
 APPLICANT: Demetrick, Douglas J.
 APPLICANT: Serrano, Manuel
 APPLICANT: Hannon, Gregory J.
 TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
 TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses

NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley, Hoag & Eliot
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordpad
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/497,214D
 FILING DATE: 30-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/346,147
 FILING DATE: 29-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/306,511
 FILING DATE: 14-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/248,812
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/227,371
 FILING DATE: 14-APR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/154,915
 FILING DATE: 18-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/991,997
 FILING DATE: 17-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: MIV-071.05
 TELEPHONE: (617) 832-1299
 TELEFAX: (617) 832-7000
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-497-214D-17
 Query Match 58.3%; Score 14; DB 3; Length 4;
 Best Local Similarity 75.0%; Pred. No. 4.1e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 KAMD 5
 Db 1 KARD 4
 RESULT 11
 US-09-016-750C-17
 Sequence 17, Application US/09016750C
 Patent No. 6486131
 GENERAL INFORMATION:
 APPLICANT: Beach, David H.
 APPLICANT: Demetrick, Douglas J.
 APPLICANT: Serrano, Manuel
 APPLICANT: Hannon, Gregory J.
 TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES
 TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-2170
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 30-JAN-1998
 APPLICATION NUMBER: US 08/016,750C
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/893,274
 FILING DATE: 15-JUL-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/306,511
 FILING DATE: 14-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/248,812
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/154,915
 FILING DATE: 18-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/991,997
 FILING DATE: 17-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/963,308
 FILING DATE: 16-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/09945
 FILING DATE: 18-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: MIV-071.13
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-016-750C-17

Query Match 58.3%; Score 14; DB 4; Length 4;
 Best Local Similarity 75.0%; Pred. No. 4.1e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMD 5
 DB 1 KARD 4

RESULT 12
 US-08-528-523-2
 Sequence 2, Application US/08528523
 Patent No. 5824782
 GENERAL INFORMATION:
 APPLICANT: Hoelzer, Wolfgang
 APPLICANT: von Hoegen, Ilka
 APPLICANT: Strittmatter, Wolfgang
 APPLICANT: Matzku, Siegfried
 TITLE OF INVENTION: Immunoconjugates II

NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
 STREET: 2200 Clarendon Boulevard, Suite 1400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/528,523
 FILING DATE: 06-NOV-1992
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 94114572.4
 FILING DATE: 16-SEP-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Hamlet-King, Diana
 REGISTRATION NUMBER: 33,302
 REFERENCE/DOCKET NUMBER: Merck 1717
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-243-6333
 TELEFAX: 703-243-6410
 TELEX: 64191
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE: internal
 US-08-528-523-2

Query Match 58.3%; Score 14; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KAM 4
 DB 1 KAM 3

RESULT 13
 US-08-933-219B-2
 Sequence 2, Application US/089333219B
 Patent No. 6329140
 GENERAL INFORMATION:
 APPLICANT: Lockhart et al.
 APPLICANT: Affymetrix, Inc.
 TITLE OF INVENTION: Identification of Molecular Sequence
 TITLE OF INVENTION: Signatures and Methods Involving the Same
 FILE REFERENCE: 3016.1
 CURRENT APPLICATION NUMBER: US/08/933,219B
 CURRENT FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/025,740
 PRIOR FILING DATE: 1996-09-19
 NUMBER OF SEQ ID NOS: 42
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic Sequence
 US-08-933-219B-2

Query Match 58.3%; Score 14; DB 3; Length 5;

Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KAM 4
|||
Db 3 KAM 5

RESULT 14

US-09-321-481-2
; Sequence 2, Application US/09321481
; Patent No. 6391550
; GENERAL INFORMATION:
; APPLICANT: Lockhart et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Identification of Molecular Sequence
; FILE REFERENCE: 3016.2
; CURRENT APPLICATION NUMBER: US/09/321,481
; CURRENT FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 08/933,219
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; OTHER INFORMATION: Synthetic Sequence
US-09-321-481-2

Query Match 58.3%; Score 14; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KAM 4
|||
Db 3 KAM 5

RESULT 15

US-09-535-852-1028
; Sequence 1028, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1028
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmoglein-1 cell adhesion recognition sequence
US-09-535-852-1028

Query Match 58.3%; Score 14; DB 4; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KAMD 5
:|:
Db 2 RALD 5

Search completed: May 26, 2005, 19:59:55
Job time : 41 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2005, 20:08:51 ; Search time 39 Seconds
(without alignments)
29.605 Million cell updates/sec

Title: US-10-047-945-4

Perfect score: 69

Sequence: 1 LKAWDPFPLWI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	39.1	7	2 A61081	tryptophyllin, bas
2	27	39.1	10	2 A36454	trypsin-modulating
3	24	34.8	8	2 S21288	lectin - potato (f
4	23	33.3	7	4 A58725	virotaxin - destro
5	21	30.4	10	2 C35389	urease (EC 3.5.1.5
6	21	30.4	10	2 B59272	peptide-N4-(N-acet
7	21	30.4	10	2 S39030	lysyl-bradykinin -
8	21	30.4	11	1 XAVI9H	bradykinin-potenti
9	20	29.0	5	2 B60274	major protein anti
10	20	29.0	8	2 S10783	enamelin f - bovin
11	20	29.0	8	2 A39308	glycine reductase
12	20	29.0	12	1 JTJGO	tremerogen A-10 -
13	20	29.0	12	2 PN0663	dytrophin-associa
14	19	27.5	9	2 B30572	T-cell receptor be
15	19	27.5	9	2 A60108	exotoxin A - Strep
16	19	27.5	9	2 S26508	collagen alpha 2(V
17	19	27.5	10	2 C30572	T-cell receptor be
18	19	27.5	11	2 D45900	complement C3b rec
19	18	26.1	4	2 I51049	metallothionein-A
20	18	26.1	8	2 S71919	alcohol dehydrogen
21	18	26.1	10	2 PC2171	triacylglycerol 11
22	18	26.1	10	2 A61007	hementin (EC 3.4.-
23	18	26.1	11	2 C61497	seed protein ws-18
24	18	26.1	12	2 A49033	T-cell receptor de
25	18	26.1	12	2 JQ2308	hypothetical 1.4K
26	18	26.1	12	2 JQ2318	hypothetical 1.4K
27	18	26.1	12	2 I58273	thyroglobulin - ra
28	18	26.1	12	2 S07436	tachykinin - Afric
29	17	24.6	7	2 S09652	hypothetical prote

ALIGNMENTS

RESULT 1

A61081

tryptophyllin, basic - Rohde's leaf frog

C;Species: Phyllomedusa rohdei (Rohde's leaf frog)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000

C;Accession: A61081

R;Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.

Int. J. Pept. Protein Res. 33, 391-395, 1989

A;Title: Isolation, structure determination and synthesis of a novel tryptophan-containing

A;Reference number: A61081

A;Accession: A61081

A;Molecule type: protein

A;Residues: 1-7 <MON>

C;Comment: The biological activity of this peptide was not determined.

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; hydroxyproline; skin

P;3/Modified site: 4-hydroxyproline (Pro) #status experimental

P;7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 39.1%; Score 27; DB 2; Length 7;

Best Local Similarity 80.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PPLWI 12

Db 2 PPSWI 6

RESULT 2

A36454

trypsin-modulating coostatic factor - yellow fever mosquito

C;Species: Aedes aegypti (yellow fever mosquito)

C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004

C;Accession: A36454; A61630

R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

FASEB J. 4, 3015-3020, 1990

A;Title: Mosquito coostatic factor: a novel decapeptide modulating trypsin-like enzyme bi.

A;Reference number: A36454; MUID:90367888; PMID:2394318

A;Accession: A36454

A;Molecule type: protein

A;Residues: 1-10 <BOR>

A;Cross-references: UNIPROT:P19425

R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

Insect Biochem. Mol. Biol. 23, 703-712, 1993

A;Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost

A;Reference number: A61630; MUID:93357794; PMID:8353526

A;Accession: A61630

A;Molecule type: protein

A;Residues: 1-10 <B02>

A;Note: none of the amino acids is modified

C;Function:

A;Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ep

leucokinin VII - M
alpha-gliadin 4Ha
alpha-gliadin 6Ha
beta-glucosidase (microbial collagen
napin small chain
Ig H chain V-D-J r
Ig H chain V-D-J r
ATP synthase D cha
lebetin 1 isoform
acid proteinase li
adipokinetic hormo
acylase - Kluyvera
angiotensin-conver
gene c-mpl protein
ATPase R1 subunit

30 17 24.6 8 2 JS0317
31 17 24.6 10 2 A61218
32 17 24.6 10 2 B61218
33 17 24.6 11 2 P00231
34 17 24.6 12 2 A26093
35 17 24.6 12 2 S70337
36 17 24.6 12 2 PH1587
37 17 24.6 12 2 PH1611
38 17 24.6 12 2 FN0046
39 17 24.6 12 2 S71380
40 16 23.2 5 2 B37988
41 16 23.2 8 2 S10596
42 16 23.2 8 2 S19288
43 16 23.2 8 2 A31570
44 16 23.2 9 2 I58350
45 16 23.2 9 2 D48186

C;Keywords: hormone

Query Match 39.1%; Score 27; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9
|||
Db 2 DPAPP 6

RESULT 3

S21288
lectin - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: S21288
R;Miller, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
Biochem. J. 283, 813-821, 1992
A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization
A;Reference number: S21288; MUID:92272683; PMID:1590771
A;Accession: S21288
A;Molecule type: protein
A;Residues: 1-8 <MIL>
A;Cross-references: UNIPROT:Q7M1V6
A;Experimental source: var. Ulster Sceptre
C;Function:
A;Description: may be involved in defence mechanism of the plant
C;Keywords: hydroxyproline; lectin

Query Match 34.8%; Score 24; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTPP 9
|||
Db 2 ASTPSPP 8

RESULT 4

A58725
virotoxin - destroying angel
C;Species: Amanita virosa (destroying angel)
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: A58725
R;Faustich, H.; Buku, A.; Bodenmuller, H.; Wieland, T.
Biochemistry 19, 334-343, 1980
A;Title: Virotoxins: actin-binding cyclic peptides of Amanita virosa mushrooms.
A;Reference number: A58725; MUID:6893271; PMID:6893271
A;Accession: A58725
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <FAU>
C;Keywords: D-amino acid; hydroxyproline; toxin; unencoded polypeptide
F1/7/Cross-link: cyclopeptide (Val-Leu) #status experimental
F2/Modified site: D-threonine (Thr) #status experimental
F3/Modified site: D-serine (Ser) #status experimental
F4/Modified site: (3R,4S)-3,4-dihydroxyproline (Pro) #status experimental
F6/Modified site: 2'-methylsulfonyltryptophan (Trp) #status experimental
F7/Modified site: 4,5-dihydroxyisoleucine (Leu) #status experimental

Query Match 33.3%; Score 23; DB 4; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 TPPLWI 12
|||
Db 2 TSPAWL 7

RESULT 5

C35389
urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)

C;Species: Morganella morganii
C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 09-Jul-2004
C;Accession: C35389
R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Bacteriol. 172, 3073-3080, 1990
A;Title: Morganella morganii urease: purification, characterization, and isolation of gene
A;Reference number: A35389; MUID:90264298; PMID:2345135
A;Accession: C35389
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <HUA>
A;Cross-references: UNIPROT:P17339
C;Keywords: hydrolase

Query Match 30.4%; Score 21; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPP 9
|||
Db 1 MQLTTP 6

RESULT 6

B59272
peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain -
N;Alternate names: peptide N-glycosidase
C;Species: Prunus dulcis var. sativa (sweet almond)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: B59272
R;Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
Eur. J. Biochem. 252, 118-123, 1998
A;Title: Characterisation of peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine amidase A
A;Reference number: A59272; MUID:98181894; PMID:9523720
A;Accession: B59272
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <ALT>
A;Cross-references: UNIPROT:P81898
C;Keywords: hydrolase

Query Match 30.4%; Score 21; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPTP 8
:|
Db 1 EPTP 4

RESULT 7

S39030
lysyl-bradykinin - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 16-Aug-2004
C;Accession: S39030
R;Conlon, J.M.; Olson, K.R.
FEBS Lett. 334, 75-78, 1993
A;Title: Purification of a vasoactive peptide related to lysyl-bradykinin from trout plasma
A;Reference number: S39030; MUID:94039817; PMID:8224232
A;Accession: S39030
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <CON>
A;Cross-references: UNIPROT:Q9PRZ1

Query Match 30.4%; Score 21; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PPLW 11
|||
Db 3 PPGW 6

```

RESULT 8
XAVIBH
bradykinin-potentiating peptide - halys viper
N:Alternate names: Bpp
C:Species: Agkistrodon halys (halys viper)
C>Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C:Accession: JC0002
R:Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.
Peptides 6, 339-342, 1985
A:Title: Structure-function studies on the bradykinin potentiating peptide from Chinese
A:Reference number: JC0002; MUID:86177022; PMID:3008123
A:Accession: JC0002
A:Molecule type: protein
A:Residues: 1-11 <CHI>
A:Cross-references: UNIPROT:P04562
C:Comment: Because this peptide both inhibits the activity of the angiotensin-converting
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyrog
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.4%; Score 21; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTPPL 10
DB 5 PGPP 9

RESULT 9
B60274
major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)
C:Species: Mycobacterium tuberculosis
C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C:Accession: B60274
R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A:Title: Isolation and partial characterization of major protein antigens in the culture
A:Reference number: A60274; MUID:91099989; PMID:1898899
A:Accession: B60274
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <NAG>

Query Match 29.0%; Score 20; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTP 8
DB 1 DPAP 4

RESULT 10
S10783
enamelin f - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S10783
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu
A:Reference number: S10780; MUID:90336641; PMID:2379503
A:Accession: S10783
A:Molecule type: protein
A:Residues: 1-8 <STR>
C:Keywords: enamel; phosphoprotein

Query Match 29.0%; Score 20; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 6 PTPP 9
DB 2 PLPP 5

RESULT 11
A39308
glycine reductase (EC 1.4.99.-) sulfhydryl protein C, alpha chain - Clostridium stickla
C:Species: Clostridium sticklandii
C>Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 09-Jul-2004
C:Accession: A39308
R:Stadtman, T.C.; Davis, J.N.
J. Biol. Chem. 266, 22147-22153, 1991
A:Title: Glycine reductase protein C. Properties and characterization of its role in th
A:Reference number: A39308; MUID:92042141; PMID:1939235
A:Accession: A39308
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <STA>
A:Cross-references: UNIPROT:Q7M0L0
C:Function:
A:Description: glycine reductase complex catalyzes the reductive deamination of glycine
C:Keywords: ATP; oxidoreductase

Query Match 29.0%; Score 20; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PPLW 11
DB 3 PVLW 6

RESULT 12
J1060
Tremorgen A-10 - jelly fungus (Tremella mesenterica)
C:Species: Tremella mesenterica
C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C:Accession: A01642; A61313
R:Sakagami, Y.; Yoshida, M.; Isogai, A.; Suzuki, A.
Science 212, 1525-1527, 1981
A:Title: Peptide sex hormones inducing conjugation tube formation in compatible mating-r
A:Reference number: A94256
A:Accession: A01642
A:Molecule type: protein
A:Residues: 1-12 <SAKI>
A:Cross-references: UNIPROT:P01371
A:Note: the farnesyl may instead be (2E,6E,10Z)-12-hydroxyfarnesyl
R:Sakagami, Y.; Isogai, A.; Suzuki, A.; Tamura, S.; Tsuchiya, E.; Fukui, S.
Agric. Biol. Chem. 42, 1301-1302, 1978
A:Title: Amino acid sequence of tremorgen A-10, a peptidal hormone, inducing conjugati
A:Reference number: A61313
A:Accession: A61313
A:Molecule type: protein
A:Residues: 1-12 <SAK2>
C:Comment: Tremorgen A-10 is produced by the A mating-type cells and induces formation
C:Superfamily: tremorgen a-13
C:Keywords: extracellular protein; hormone; lipoprotein; methylated carboxyl end; pherom
F:12/Binding site: farnesyl (Cys) (covalent) #status experimental
F:12/Modified site: methyl ester carboxyl end (Cys) #status experimental

Query Match 29.0%; Score 20; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPP 9
DB 3 DPSAP 7

RESULT 13
PN0663

```

Search completed: May 26, 2005, 20:18:24
Job time : 41 secs

dystrophin-associated glycoprotein A3a-II - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C:Accession: PN0663
R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993
A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained
A:Reference number: PN0662; MUID:94156881; PMID:8113213
A:Accession: PN0663
A:Molecule type: protein
A:Residues: 1-12 <YOS>
C:Comment: this protein is retained in Duchenne type muscular dystrophy muscle.
C:Keywords: glycoprotein; skeletal muscle

Query Match 29.0%; Score 20; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 FTTP 9
|||
Db 3 PLPP 6

RESULT 14
B30572
T-cell receptor beta chain C region (CRNB29) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Apr-1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997
C:Accession: B30572
R;Williams, C.B.; Gutman, G.A.
J. Immunol. 142, 1027-1035, 1989
A:Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utilization
A:Reference number: A30563; MUID:89110038; PMID:2563271
A:Accession: B30572
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-9 <WIL>
C:Keywords: T-cell receptor

Query Match 27.5%; Score 19; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TPP 9
|||
Db 7 TPP 9

RESULT 15
A60108
exotoxin A - Streptococcus pyogenes (strain C203.S) (fragment)
N:Alternate names: blastogen A; scarlet fever toxin
C:Species: Streptococcus pyogenes
C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C:Accession: A60108
R;Schlievert, P.M.; Gray, E.D.
Infect. Immun. 57, 1865-1867, 1989
A:Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and blast
A:Reference number: A60108; MUID:89254013; PMID:2498210
A:Accession: A60108
A:Molecule type: protein
A:Residues: 1-9 <SCH>
A:Cross-references: UNIPROT:Q54779; UNIPROT:P97163; UNIPROT:Q9R931; UNIPROT:Q57453; UNIP
C:Keywords: exotoxin

Query Match 27.5%; Score 19; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DFTP 8
|||
Db 2 DPDP 5

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OM protein - protein search, using sw model

Run on: May 26, 2005, 20:00:51 ; Search time 171 Seconds
(without alignments)
35.935 Million cell updates/sec

Title: US-10-047-945-4

Perfect score: 69

Sequence: 1 LKANDPTPLWI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 4233

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	39.1	7	1 TPFY_PACDA	P83455 pachymedusa
2	27	39.1	10	1 TMOF_AEDAE	P19425 aedes aegypti
3	26	37.7	11	2 Q9UCR1	Q9UCR1 homo sapien
4	25	36.2	12	2 Q6X7V1	Q6X7V1 canis famill
5	25	36.2	12	2 Q8KZ86	Q8KZ86 acinetobact
6	24	34.8	8	2 Q7M1V6	Q7M1V6 solanum tub
7	23	33.3	10	2 Q76MK5	Q76MK5 eurypharynx
8	23	33.3	11	2 Q81VGS	Q81VGS homo sapien
9	22	31.9	11	2 Q8MA21	Q8MA21 maripa pani
10	22	31.9	11	2 Q8MA23	Q8MA23 maripa repe
11	22	31.9	11	2 Q8MB39	Q8MB39 wilsonia hu
12	22	31.9	11	2 Q8MB58	Q8MB58 seddera hir
13	22	31.9	11	2 Q8MB77	Q8MB77 odonellia h
14	22	31.9	11	2 Q8MB79	Q8MB79 aniseia arg
15	22	31.9	11	2 Q8MB97	Q8MB97 merremia pe
16	22	31.9	11	2 Q8MBE1	Q8MBE1 ipomoea alb
17	21	30.4	6	1 E101_LITRU	P82096 litorea rub
18	21	30.4	9	2 Q9H326	Q9H326 homo sapien
19	21	30.4	9	2 Q6SP94	Q6SP94 chlamydomon
20	21	30.4	9	2 Q99193	Q99193 pseudomonas
21	21	30.4	9	2 Q9PRJ4	Q9PRJ4 lepisosteus
22	21	30.4	10	1 BRK_ONCMY	Q9PRZ1 oncorhynch
23	21	30.4	10	1 PNAS_PRUDU	P81898 prunus dulc
24	21	30.4	10	1 URE3_MORMO	P17339 morganelia
25	21	30.4	10	2 Q67BK2	Q67BK2 klebsiella
26	21	30.4	11	1 BPP_AGKHP	P04562 agkistrodon
27	21	30.4	11	2 Q77896	Q77896 oreochromis
28	21	30.4	12	2 Q47251	Q47251 escherichia
29	20	29.0	7	1 UF04_MOUSE	P36642 mus musculu
30	20	29.0	8	2 Q7M0L0	Q7M0L0 clostridium
31	20	29.0	10	2 Q91WZ3	Q91WZ3 rattus sp.

32	20	29.0	10	2	Q75595	human immun
33	20	29.0	11	2	Q9HCNS	Q9HCNS homo sapien
34	20	29.0	12	1	TA10_TREME	P01371 tremella me
35	20	29.0	12	2	Q9BZ49	Q9BZ49 homo sapien
36	20	29.0	12	2	Q7YNG6	Q7YNG6 salicornia
37	19	27.5	8	2	Q6LDP8	Q6LDP8 pseudomonas
38	19	27.5	8	2	Q9ET16	Q9ET16 mesocricetu
39	19	27.5	8	2	Q9ET17	Q9ET17 mus caroli
40	19	27.5	8	2	Q9ET18	Q9ET18 mus spretus
41	19	27.5	9	2	Q7M2M9	Q7M2M9 bos taurus
42	19	27.5	10	1	PAR5_MACRS	P83278 macrobrachi
43	19	27.5	10	1	UHA3_HUMAN	P49930 homo sapien
44	19	27.5	10	2	Q8VHM9	Q8VHM9 mus musculu
45	19	27.5	10	2	Q9ESU5	Q9ESU5 mus musculu

ALIGNMENTS

RESULT 1

ID TPFY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Trypophyllin-1 (Pdt-1)
OS Pachymedusa dactylosa (Giant Mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RT "Pachymedusa dactylosa tryptophyllin-1 (Pdt-1): structural
characterization, pharmacological activity and cloning of precursor
cDNA";
RL Submitted (SEP-2002) to Swiss-Prot.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI; RANGE=1-7; NOTE=Ref.1.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.
KW Amidation; Amphibian defense peptide; Direct protein sequencing;
KW Hydroxylation.
FT MOD_RES 3 3 Hydroxyproline.
FT MOD_RES 7 7 Proline amide.
SQ SEQUENCE 7 AA, 794 MW; 7772D37DC776350 CRC64;

Query Match 39.1%; Score 27; DB 1; Length 7;

Best Local Similarity 60.0%; Pred. No. 1.6e+06;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PPLWI 12

Db 2 PPAWV 6

RESULT 2

ID TMOF_AEDAE STANDARD; PRT; 10 AA.
AC P19425;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DB Trypsin-modulating oostatic factor (TMOF) (OOSH).
OS Aedes aegypti (Yellow fever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
 RN NCBI_TaxID=7159;
 RP SEQUENCE.
 RC STRAIN=Vero beach; TISSUE=Ovary;
 RX MEDLINE=90367888; PubMed=2394318;
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
 RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like
 RT enzyme biosynthesis in the midgut."
 RN FASEB J. 4:3015-3020 (1990).
 RP SEQUENCE.
 RC STRAIN=Vero beach; TISSUE=Ovary;
 RX MEDLINE=93357794; PubMed=8353526; DOI=10.1016/0956-1748(93)90044-S;
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
 RT "Mass spectrometry and characterization of Aedes aegypti trypsin
 RT modulating oostatic factor (TMOF) and its analogs."
 RL Insect Biochem. Mol. Biol. 23:703-712 (1993).
 CC -!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
 CC in the midgut which indirectly reduces the vitellogenin
 CC concentration in the hemolymph resulting in inhibition of oocyte
 CC development.
 CC -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular
 CC epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs
 CC and stops at 56 hrs.
 DR PIR; A36454; A36454.
 KW Direct protein sequencing; Hormone.
 FT DOMAIN 3 10 Poly-Pro.
 FT VARIANT 1 2 YD -> DY (in TMOF(B)).
 SQ SEQUENCE 10 AA; 1047 MW; 236D0A777776DC7 CRC64;

Query Match 39.1%; Score 27; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 9.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTTP 9
 ||||
 Db 2 DPAPP 6

RESULT 3
 Q9UCR1 PRELIMINARY; PRT; 11 AA.
 AC Q9UCR1;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE AUTOTAXIN (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92129337; PubMed=1733949;
 RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
 RA Schiffmann E., Liotta L.A.;
 RT "Identification, purification, and partial sequence analysis of
 RT autotaxin, a novel motility-stimulating protein."
 RL J. Biol. Chem. 267:2524-2529 (1992).
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1171 MW; 2723615AA0437737 CRC64;

Query Match 37.7%; Score 26; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PLWI 12
 ||||
 Db 4 PLWI 7

RESULT 4
 Q6X7V1 PRELIMINARY; PRT; 12 AA.
 AC Q6X7V1;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Insulin-like factor 3 (Fragment).
 GN Name=INSL3;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22929740; PubMed=12890727;
 RA Truong A., Bogatcheva N.V., Schelling C., Dolf G., Agouluk A.I.;
 RT "Isolation and expression analysis of the canine insulin-like factor 3
 RT gene."
 RL Biol. Reprod. 69:1658-1664 (2003).
 DR EMBL; AY251015; AAP79619.1; -.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1354 MW; 20ED91ADFA7DD737 CRC64;

Query Match 36.2%; Score 25; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 2.5e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 MDPTPLW 11
 ||||
 Db 1 MSPRPLAW 8

RESULT 5
 Q8KZ86 PRELIMINARY; PRT; 12 AA.
 AC Q8KZ86;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Class I integron DNA integrase (Fragment).
 GN Name=intI1;
 OS Acinetobacter baumannii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=470;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22270987; PubMed=12384388;
 RA Gombac F., Riccio M.L., Rossolini G.M., Lagatolla C., Tonin E.,
 RA Monti-Bragadin C., Lavenia A., Dolzani L.;
 RT "Molecular characterization of integrons in epidemiologically
 RT unrelated clinical isolates of Acinetobacter baumannii from Italian
 RT hospitals reveals a limited diversity of gene cassette arrays."
 RL Antimicrob. Agents Chemother. 46:3665-3668 (2002).
 DR EMBL; AJ313333; CAC85941.1; -.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1296 MW; 90426B8F5E376DC1 CRC64;

Query Match 36.2%; Score 25; DB 2; Length 12;
 Best Local Similarity 62.5%; Pred. No. 2.5e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AMDPTPL 10
 ||||
 Db 4 ATAPLPL 11

RESULT 6
 Q7M1V6 PRELIMINARY; PRT; 8 AA.
 AC Q7M1V6;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)

```

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lectin (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamnids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RA Millar D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R.,
RA Bolwell G.P.;
RT "Chitin-binding proteins in potato (Solanum tuberosum L.) tuber.
RT Characterization, immunolocalization and effects of wounding.";
RL Biochem. J. 283:813-821(1992).
DR PIR; S21288; S21288.
FT NON_TER 1
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 771 MW; C37775A771BSBDDA CRC64;

Query Match 34.8%; Score 24; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AMDTPP 9
Db 2 ASTESP 8

RESULT 7
Q76MKS PRELIMINARY; PRT; 10 AA.
AC Q76MKS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Atpase subunit 8 (Fragment).
GN Name=Atpase 8;
OS Eurypharynx pelicanoides (pelican eel).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
OX NCBI_TaxID=55117;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22967687; PubMed=12949142; DOI=10.1093/molbev/msg206;
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
RT scale gene rearrangements originated within the eels.";
RL Mol. Biol. Evol. 20:1917-1924(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046487; BAB87160.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;

Query Match 33.3%; Score 23; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDTPP 8
Db 4 LDSP 8

RESULT 8
Q81VGB PRELIMINARY; PRT; 11 AA.
ID Q81VGB

```

```

AC Q81VGB;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Low density lipoprotein receptor related protein 1 (Lipoprotein
DE receptor-related protein) (Fragment).
GN Name=LRP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Glaeser C.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Schulz S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=90089395; PubMed=2597675;
RA Kuett H.C., Herz J., Stanley K.K.;
RT "Structure of the low-density lipoprotein receptor-related protein
RT (LRP) promoter.";
RL Biochim. Biophys. Acta 1009:229-236(1989).
DR EMBL; Y18524; CAD57169.1; -.
DR EMBL; X15424; CAA33464.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Lipoprotein; Receptor.
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1221 MW; 373D041E27273777 CRC64;

Query Match 33.3%; Score 23; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TPPL 10
Db 3 TPPL 6

RESULT 9
Q8MAZI PRELIMINARY; PRT; 11 AA.
AC Q8MAZI;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Pbbj (Fragment).
GN Name=psbj;
OS Maripa paniculata.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamnids; Solanales; Convolvulaceae; Maripaeae; Maripa.
OX NCBI_TaxID=197411;
RN [1]
RP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 89:1510-1522(2002).
DR EMBL; AY100937; AAM55869.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 31.9%; Score 22; DB 2; Length 11;

```

```

Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy . 9 PLW 11
    |||
Db 9 PLW 11

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```

RESULT 10
Q8MAZ3 PRELIMINARY; PRT; 11 AA.
ID Q8MAZ3
AC Q8MAZ3;
DT 01-OCT-2002 ('TrEMBLrel. 22, Created)
DT 01-OCT-2002 ('TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 ('TrEMBLrel. 24, Last annotation update)
DE FebJ (Fragment).
OS Maripa repens; GN Name=psbj;
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamnids; Solanales; Convolvulaceae; Maripaeae; Maripa.
NCBI_TaxID=197412; [1]
SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RP "Monophyly of the Convolvulaceae and circumscription of their major
RT lineages based on DNA sequences of multiple chloroplast loci.";
RL Am. J. Bot. 89;1510-1522(2002).
DR EMBL; AY100936; XMS5865.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match          31.9%; Score 22; DB 2; Length 11;
Best Local Similarity 100.0%; Pred.No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	9 PLW 11
D _b	9 PLW 11

[illegible]

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PLW 11
        |||
Db      9 PLW 11

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RESULT	ID	Q8MB58	PRELIMINARY;	PRT;	11 AA.
AC	Q8MB58;				
AD	01-OCT-2002 (TrEMBLrel. 22, Created)				
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DE	PsbJ (Fragment).				
DE	Name=psbj;				
OS	Seddera hirsuta.				
OS	Chloroplast.				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Opisthokonta; Magnoliophyta; eudicotyledons; core eudicots; asterids;				
OC	Lamiids; Solanales; Convolvulaceae; Cresseae; Seddera.				
OC	NCBI_TaxID=197444;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Stefanovic S., Krueger L., Olmstead R.G.;				
RT	Monophyly of the Convolvulaceae and circumscription of their major				
RT	lineages based on DNA sequences of multiple chloroplast loci.";				
RL	Am. J. Bot. 89:1510-1523(2002).				
DR	ENBL; AY100905; AM55743.1; -.				
DR	GO; GO:0009507; C:chloroplast; IEA.				
FT	Chloroplast.				
KW	NON TER				
FT	11				
SQ	SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;				

Query Match	Best Local Similarity	31.9%;	Score 22;	DB 2;	Length 11;
Matches 3;	Conservative	100.0%;	Pred.No. 6.9e+03;		
			0; Mismatches	0; Indels	0; Gaps

Qy	9 PLW 11
Db	9 PLW 11

RESULT	13
Q8MB77	PRELIMINARY; PRT; 11 AA.
ID	Q8MB77;
AC	Q8MB77;
DT	01-OCT-2002 (TREMBLrel. 22, Created)
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	PebJ (Fragment).
GN	Name=psbj;
OS	-Odonellia hirtiflora.
OG	Chloroplast.
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC	Lamids; Solanales; Convolvulaceae; Anisiaceae; Odonellia.
OX	NCBI_TaxID:197424;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Stefanovic S., Krueger L., Olmstead R.G.;
RT	"Monophyly of the Convolvulaceae and circumscription of their major
RT	lineages based on DNA sequences of multiple chloroplast loci.";
RL	Am. J. Bot. 89:1510-1522(2002).
DR	EMBL; AY100897; AAM55711.1; -.
DR	GO; GO:0009507; C:chloroplast; IEA.
KW	Chloroplast.
FT	NON TER 11 11
SQ	SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;
Query Match	31.9%; Score 22; DB 2; Length 11;
Best Local Similarity	100.0%; Pred.No. 6.9e+03;
Matches 3; Conservative	0; Mismatches 0; Indels 0; Gaps

Qy 9 PLW 11
 |||
 Db 9 PLW 11

Qy 9 PLW 11
 |||
 Db 9 PLW 11

Search completed: May 26, 2005, 20:17:51
 Job time : 185 secs

RESULT 14

Q8MB79 PRELIMINARY; PRT; 11 AA.
 AC Q8MB79;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE P8bJ (Fragment).
 GN Name=p8bJ;
 OS Aniseia argentina.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamids; Solanales; Convolvulaceae; Anisaleae; Aniseia.
 OX NCBI_TaxID=197349;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 lineages based on DNA sequences of multiple chloroplast loci.";
 RL Am. J. Bot. 89:1510-1522(2002).
 DR EMBL; AY100895; AAMS5703.1; "-"
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 31.9%; Score 22; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PLW 11
 |||
 Db 9 PLW 11

RESULT 15

Q8MB97 PRELIMINARY; PRT; 11 AA.
 AC Q8MB97;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE P8bJ (Fragment).
 GN Name=p8bJ;
 OS Merremia peltata.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamids; Solanales; Convolvulaceae; Merremieae; Merremia.
 OX NCBI_TaxID=197416;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stefanovic S., Krueger L., Olmstead R.G.;
 RT "Monophyly of the Convolvulaceae and circumscription of their major
 lineages based on DNA sequences of multiple chloroplast loci.";
 RL Am. J. Bot. 89:1510-1522(2002).
 DR EMBL; AY100895; AAMS5663.1; "-"
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1260 MW; 93736D59440861B1 CRC64;

Query Match 31.9%; Score 22; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 20:00:02 ; Search time 159 Seconds
(without alignments)
29.189 Million cell updates/sec

Title: US-10-047-945-4

Perfect score: 69

Sequence: 1 LKAWDPPTPLWI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 520583

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	69	100.0	12	7	ABB80225	Abb80225	Synthetic
2	65	94.2	11	7	ABB80226	Abb80226	Synthetic
3	54	78.3	10	2	AAW53843	Aaw53843	N-Terminu
4	54	78.3	10	7	ABB80222	Abb80222	Synthetic
5	50	72.5	9	7	ABB80227	Abb80227	Synthetic
6	43	62.3	8	7	ABB80228	Abb80228	Synthetic
7	41	59.4	9	6	ABR12621	Abri12621	Human can
8	41	59.4	9	6	ABR12017	Abri12017	Human can
9	41	59.4	9	6	ABR12854	Abri12854	Human can
10	41	59.4	10	6	ABR12743	Abri12743	Human can
11	41	59.4	10	6	ABR11875	Abri11875	Human can
12	41	59.4	10	6	ABR12121	Abri12121	Human can
13	41	59.4	10	6	ABR12948	Abri12948	Human can
14	41	59.4	10	6	ABR12106	Abri12106	Human can
15	41	59.4	10	6	ABR12294	Abri12294	Human can
16	41	59.4	10	6	ABR12738	Abri12738	Human can
17	38	55.1	9	2	AAW21252	Aaw21252	Hydroxyme
18	37	53.6	9	6	ABR11778	Abri11778	Human can
19	37	53.6	9	6	ABR12206	Abri12206	Human can
20	37	53.6	10	6	ABR12924	Abri12924	Human can
21	37	53.6	10	8	ADO64358	Ado64358	Human 213
22	36	52.2	9	6	ABR12770	Abri12770	Human can
23	36	52.2	9	6	ABR12969	Abri12969	Human can
24	36	52.2	9	6	ABR12458	Abri12458	Human can
25	36	52.2	9	6	ABR12601	Abri12601	Human can

26	36	52.2	9	6	ABR12046	Abri12046	Human can
27	36	52.2	9	6	ABR12234	Abri12234	Human can
28	36	52.2	9	8	ADO72393	Ado72393	Human 213
29	36	52.2	9	8	ADO72483	Ado72483	Human 213
30	36	52.2	9	8	ADO72536	Ado72536	Human 213
31	36	52.2	9	8	ADO72664	Ado72664	Human 213
32	36	52.2	9	8	ADO72353	Ado72353	Human 213
33	36	52.2	9	8	ADO72482	Ado72482	Human 213
34	36	52.2	9	8	ADO64670	Ado64670	Human 213
35	36	52.2	9	8	ADO65216	Ado65216	Human 213
36	36	52.2	9	8	ADO67376	Ado67376	Human 213
37	36	52.2	9	8	ADO72238	Ado72238	Human 213
38	36	52.2	9	8	ADO64109	Ado64109	Human 213
39	36	52.2	9	8	ADO65758	Ado65758	Human 213
40	36	52.2	9	8	ADO67387	Ado67387	Human 213
41	36	52.2	9	8	ADO72320	Ado72320	Human 213
42	36	52.2	9	8	ADO72329	Ado72329	Human 213
43	36	52.2	9	8	ADO64657	Ado64657	Human 213
44	36	52.2	9	8	ADO65214	Ado65214	Human 213
45	36	52.2	9	8	ADO65785	Ado65785	Human 213

ALIGNMENTS

RESULT 1
ABB80225
ID ABB80225 standard; peptide; 12 AA.
XX
AC ABB80225;
XX
DT 06-NOV-2003 (first entry)
XX
DE Synthetic LTNP, LT-12.
XX
KW Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW saliva; ELISA.
XX
OS Synthetic.
XX
PN WO2003060471-A2.
XX
PD 24-JUL-2003.
XX
PF 14-JAN-2003; 2003WO-US001044.
XX
PR 14-JAN-2002; 2002US-00047945.
XX
PA (LIPP/) LIPPS B V.
PA (LIPP/) LIPPS F W.
XX
PI Lipps BV, Lipps FW;
XX WPI; 2003-636703/60.
XX
DR Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
XX insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT asthma or diabetes, by employing an ELISA on a saliva sample from a
PT patient.
XX
PS Claim 7; Page 4; 24pp; English.
XX
CC The sequences given in ABB80222-28 represent lethal toxin neutralising
CC factor (LTNP) peptides which may be used for reducing elevated levels of
CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA) in
CC particular, the methods of the invention are useful for diagnosing and
CC treating conditions with elevated serum IGE levels, e.g. asthma,
CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid

CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX Sequence 12 AA;
 SQ

Query Match 100.0%; Score 69; DB 7; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWI 12
 |||||
 DB 1 LKAMDPTPLWI 12

RESULT 2
 ABB80226
 ID ABB80226 standard; peptide; 11 AA.

XX AC ABB80226;

XX DT 06-NOV-2003 (first entry)

XX DE Synthetic LTNF, LT-11.

XX KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.

XX OS Synthetic.

XX PN WO2003060471-A2.

XX PD 24-JUL-2003.

XX PF 14-JAN-2003; 2003WO-US001044.

XX PR 14-JAN-2002; 2002US-00047945.

XX PA (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.

XX PI Lipps BV, Lipps FW;

XX DR WPI; 2003-636703/60.

XX PT Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

XX PS Claim 7; Page 4; 24pp; English.

XX CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by

CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX Sequence 11 AA;

Query Match 94.2%; Score 65; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLW 11
 |||||
 DB 1 LKAMDPTPLW 11

RESULT 3

AAW53843

ID AAW53843 standard; peptide; 10 AA.

XX AC AAW53843;

XX DT 08-JUL-1998 (first entry)

XX DE N-terminus of opossum LTNF.

XX KW LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;
 KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
 KW histamine reaction treatment.

XX OS Didelphis virginiana.

XX PN US5744449-A.

XX PD 28-APR-1998.

XX PF 03-JUN-1996; 96US-00657163.

XX PR 10-MAY-1993; 93US-00058387.

XX PR 22-SEP-1994; 94US-00310340.

XX PA (LIPP/) LIPPS B V.

PA (LIPP/) LIPPS F W.

XX PI Lipps FW, Lipps BV;

XX DR WPI; 1998-271108/24.

XX PT Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
 PT venom(s) from all major families of poisonous snakes.

XX PS Claim 7; Col 11; 11pp; English.

XX CC This sequence represents the peptide of the invention. It is a Lethal
 CC Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic
 CC protein derived from an opossum. The peptide can be used in a method for
 CC treating a victim of envenomation from a poisonous snake, preferably a
 CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
 CC is useful for the treatment of snake bites, sepsis, allergies caused by
 CC the environment and treatment of bee or scorpion stings or toxicities
 CC caused by plant or bacterial toxins. The peptide can also be used in
 CC histamine reaction treatment. The peptide can be used in envenomation
 CC treatment for a variety of snakes without prior identification of the
 CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins

XX Sequence 10 AA;

SQ

Query Match 78.3%; Score 54; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.067;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10
 |||||
 Db 1 LKAMDPTPPL 10

RESULT 4
 ABB80222
 ID ABB80222 standard; peptide; 10 AA.
 XX
 AC ABB80222;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Synthetic LTNP, LT-10.
 XX
 KW Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.
 XX
 FN WO2003060471-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 14-JAN-2003; 2003WO-US001044.
 XX
 PR 14-JAN-2002; 2002US-00047945.
 XX
 PA (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.
 XX
 PI Lipps BV, Lipps FW;
 XX
 DR WPI; 2003-636703/60.
 XX
 PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 XX
 PS Claim 7; Page 3; 24pp; English.
 XX
 CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IgE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

Sequence 10 AA;
 SQ

Query Match 78.3%; Score 54; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.067;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 9
 |||||

Qy 1 LKAMDPTPPL 10
 |||||
 Db 1 LKAMDPTPPL 10

RESULT 5
 ABB80227
 ID ABB80227 standard; peptide; 9 AA.
 XX
 AC ABB80227;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Synthetic LTNP, LT-9.
 XX
 KW Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.
 XX
 FN WO2003060471-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 14-JAN-2003; 2003WO-US001044.
 XX
 PR 14-JAN-2002; 2002US-00047945.
 XX
 PA (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.
 XX
 PI Lipps BV, Lipps FW;
 XX
 DR WPI; 2003-636703/60.
 XX
 PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 XX
 PS Claim 7; Page 4; 24pp; English.
 XX
 CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IgE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

Sequence 9 AA;
 SQ

Query Match 72.5%; Score 50; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 9
 |||||

Db 1 LKAMDPTTP 9

RESULT 6

ABB80228
ID ABB80228 standard; peptide; 8 AA.

XX AC ABB80228;

XX DT 06-NOV-2003 (first entry)

XX DE Synthetic LTNF, LT-8.

XX KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
XX KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
XX KW ADA; achma; diabetes; autoimmune disease; systemic lupus erythematosus;
XX KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
XX KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
XX KW saliva; ELISA.

XX OS Synthetic.

XX PN WO2003060471-A2.

XX PD 24-JUL-2003.

XX PF 14-JAN-2003; 2003WO-US001044.

XX PR 14-JAN-2002; 2002US-00047945.

XX PA (LIPP/) LIPPS B V.

XX PA (LIPP/) LIPPS F W.

XX PI Lipps BV, Lipps FW;

XX DR WPI; 2003-636703/60.

XX PT Assaying a human endogenous protein (e.g. IgG, nerve growth factor,
PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT asthma or diabetes, by employing an ELISA on a saliva sample from a
PT patient.

XX PS Claim 7; Page 4; 24pp; English.

XX CC The sequences given in ABB80222-28 represent lethal toxin neutralising
CC factor (LTNF) peptides which may be used for reducing elevated levels of
CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
CC particular, the methods of the invention are useful for diagnosing and
CC treating conditions with elevated serum IgE levels, e.g. asthma,
CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
CC the protein may be monitored by assaying a human endogenous protein by
CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
CC sample using an anti-serum that is specific for the protein. Saliva
CC collection is relatively non-invasive when compared to blood collection
CC for serum. Saliva can be centrifuged immediately, whereas blood requires
CC clotting time before centrifugation to separate serum. Saliva proteins
CC can be assayed by a simple ELISA test, whereas an assay of proteins from
CC serum requires a more complicated sandwich type ELISA

XX SQ Sequence 8 AA;

Query Match 62.3%; Score 43; DB 7; Length 8;

Best Local Similarity 100.0%; Pred. NO. 1.8e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTTP 8

Db 1 LKAMDPTTP 8

RESULT 7

ABR12621
ID ABR12621 standard; peptide; 9 AA.

XX AC ABR12621;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 156PID4 HLA peptide #856.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US011654.

XX PR 10-APR-2001; 2001US-0282739P.

XX PR 10-APR-2001; 2001US-0283112P.

XX PR 25-APR-2001; 2001US-0286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.

XX PS Claim 13; Page 238; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic agents. The proteins and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention

XX SQ Sequence 9 AA;

Query Match 59.4%; Score 41; DB 6; Length 9;

Best Local Similarity 66.7%; Pred. NO. 1.8e+06;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 MDPTPLPW 12

Db 1 MDPSVPIWI 9

RESULT 8

ABR12017
ID ABR12017 standard; peptide; 9 AA.

XX AC ABR12017;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 156PID4 HLA peptide #252.


```

DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 239; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 10 AA;
Query Match 59.4%; Score 41; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 MDPTPLWI 12
DB 1 MDPSVPIWI 9
||||:|:|

RESULT 11
ABR11875
ID ABR11875 standard; peptide; 10 AA.
XX
AC ABR11875;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 156P1D4 HLA peptide #110.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
WPI; 2003-075555/07.
XX
New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 231; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
XX
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 10 AA;
Query Match 59.4%; Score 41; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 MDPTPLWI 12
DB 1 MDPSVPIWI 9
||||:|:|

RESULT 12
ABR12121
ID ABR12121 standard; peptide; 10 AA.
XX
AC ABR12121;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 156P1D4 HLA peptide #356.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
WPI; 2003-075555/07.
XX
New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 233; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 10 AA;
Query Match 59.4%; Score 41; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 MDPTPLWI 12
DB 2 MDPSVPIWI 10
||||:|:|

```

```

CC from the invention
XX Sequence 10 AA;
SQ

Query Match          59.4%; Score 41; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDPTPLWI 12
Db 1 MDPSVPIWI 9
|||: |||

RESULT 13
ABR12948
ID ABR12948 standard; peptide; 10 AA.
XX ABR12948;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 156P1D4 HLA peptide #1183.
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
FN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0283112P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 241; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 10 AA;

Query Match          59.4%; Score 41; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDPTPLWI 12
Db 1 MDPSVPIWI 9
|||: |||

RESULT 14
ABR12106
ID ABR12106 standard; peptide; 10 AA.
XX ABR12106;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 156P1D4 HLA peptide #341.
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
FN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0283112P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 233; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 10 AA;

Query Match          59.4%; Score 41; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDPTPLWI 12
Db 2 MDPSVPIWI 10
|||: |||

RESULT 15
ABR12294
ID ABR12294 standard; peptide; 10 AA.
XX ABR12294;
XX
DT 19-MAY-2003 (first entry)

```

XX Human cancer-related protein 156P1D4 HLA peptide #529.
DE Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX Homo sapiens.
XX OS
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Rid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX Claim 13; Page 235; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX Sequence 10 AA;
SQ
Query Match 59.4%; Score 41; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 MDPTPLWI 12
DB 2 MDPSVPIWI 10
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Job time : 162 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 20:18:00 ; Search time 134 Seconds
(without alignments)
30.893 Million cell updates/sec

Title: US-10-047-945-4

Perfect score: 69

Sequence: 1 LKAMDPTPLWI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 214676

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Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	69	100.0	12	US-10-047-945-4
2	65	94.2	11	US-10-047-945-5
3	54	78.3	10	US-10-047-945-1
4	50	72.5	9	US-10-047-945-6
5	43	62.3	8	US-10-047-945-7
6	38	55.1	9	US-10-930-300-52
7	34	49.3	12	US-10-327-598-735
8	32	46.4	12	US-10-185-815-6
9	32	46.4	12	US-10-161-791-252
10	32	46.4	12	US-10-116-275-52
11	31	44.9	9	US-10-611-440-188
12	30	43.5	8	US-10-437-708-168
13	30	43.5	8	US-10-418-032-168

14	30	43.5	10	14	US-10-190-082-480	Sequence 480, App
15	30	43.5	10	15	US-10-437-708-165	Sequence 165, App
16	30	43.5	10	17	US-10-418-032-165	Sequence 165, App
17	30	43.5	12	14	US-10-325-567A-2288	Sequence 2288, App
18	29	42.0	9	10	US-09-935-430-7	Sequence 7, Appli
19	29	42.0	9	14	US-10-277-292-7	Sequence 7, Appli
20	29	42.0	9	15	US-10-280-340-7	Sequence 7, Appli
21	29	42.0	9	15	US-10-057-475B-10870	Sequence 10870, A
22	29	42.0	9	15	US-10-057-475B-10923	Sequence 10923, A
23	29	42.0	9	15	US-10-057-475B-10929	Sequence 10929, A
24	29	42.0	9	15	US-10-154-884B-10870	Sequence 10870, A
25	29	42.0	9	15	US-10-154-884B-10923	Sequence 10923, A
26	29	42.0	9	15	US-10-154-884B-10929	Sequence 10929, A
27	29	42.0	10	10	US-09-935-430-74	Sequence 74, Appl
28	29	42.0	10	14	US-10-277-292-74	Sequence 74, Appl
29	29	42.0	10	14	US-10-277-292-619	Sequence 619, App
30	29	42.0	10	14	US-10-280-340-74	Sequence 74, Appl
31	29	42.0	10	15	US-10-280-340-619	Sequence 619, App
32	29	42.0	10	15	US-10-185-815-1	Sequence 1, Appli
33	29	42.0	12	14	US-10-235-175-18	Sequence 18, Appl
34	29	42.0	12	14	US-10-116-275-47	Sequence 47, Appl
35	29	42.0	12	15	US-08-344-824-273	Sequence 273, App
36	28	40.6	9	8	US-08-344-824-361	Sequence 361, App
37	28	40.6	10	8	US-09-739-852-7	Sequence 7, Appli
38	28	40.6	10	9	US-10-286-457-136	Sequence 136, App
39	28	40.6	12	14	US-10-808-187-1161	Sequence 1161, Ap
40	27	39.1	4	17	US-09-870-498A-8	Sequence 8, Appli
41	27	39.1	7	10	US-09-758-128-20	Sequence 20, Appl
42	27	39.1	8	9	US-09-758-128-23	Sequence 23, Appl
43	27	39.1	8	9	US-09-758-128-26	Sequence 26, Appl
44	27	39.1	8	9	US-09-758-128-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1

US-10-047-945-4
; Sequence 4, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT01505
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.
US-10-047-945-4

Query Match 100.0%; Score 69; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWI 12

Db 1 LKAMDPTPLWI 12

RESULT 2

US-10-047-945-5

```

; Sequence 5, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.
US-10-047-945-5

```

```

Query Match      94.2%; Score 65; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 LKAMDPTPLW 11
        |||||
DB      1 LKAMDPTPLW 11

```

RESULT 3

```

US-10-047-945-1
; Sequence 1, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-1

```

```

Query Match      78.3%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 LKAMDPTPL 10
        |||||
DB      1 LKAMDPTPL 10

```

RESULT 4

```

US-10-047-945-6
; Sequence 6, Application US/10047945

```

```

; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.
US-10-047-945-6

```

```

Query Match      72.5%; Score 50; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 LKAMDPTPP 9
        |||||
DB      1 LKAMDPTPP 9

```

RESULT 5

```

US-10-047-945-7
; Sequence 7, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
US-10-047-945-7

```

```

Query Match      62.3%; Score 43; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 LKAMDPTP 8
        |||||
DB      1 LKAMDPTP 8

```

RESULT 6

```

US-10-930-300-52
; Sequence 52, Application US/10930300
; Publication No. US20050014138A1
; GENERAL INFORMATION:
; APPLICANT: Rath, Matthias

```


;; TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL
;;
;; NUMBER OF SEQUENCES: 360
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: INHOUSE IP MANAGEMENT
;; STREET: 280 Colorado Avenue
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94301
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: WINDOWS 95
;; SOFTWARE: MS WORD 6.0
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/930,300
;; FILING DATE: 30-AUG-2004
;; CLASSIFICATION: <unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/182,248
;; FILING DATE: 14-JAN-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ALI KAMAREI
;; REGISTRATION NUMBER: 37000
;; REFERENCE/DOCKET NUMBER: 10262-1US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-322-7371
;; TELEFAX: 650-322-7389
;; INFORMATION FOR SEQ ID NO: 52:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-930-300-52

Query Match 55.1%; Score 38; DB 17; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPLW 11
Db 1 DPTPLW 7

RESULT 7
US-10-327-598-735
; Sequence 735, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 735
; LENGTH: 12
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-735

Query Match 49.3%; Score 34; DB 16; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTTP 9
Db 1 QSPDPTTP 8

RESULT 8
US-10-185-815-6
; Sequence 6, Application US/10185815
; Publication No. US20030096354A1
; GENERAL INFORMATION:
; APPLICANT: Elan Corporation, plc
; APPLICANT: O'Mahony, Daniel
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands
; FILE REFERENCE: E1067-20093
; CURRENT APPLICATION NUMBER: US/10/185,815
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/302,591
; PRIOR FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polypeptide ligand
US-10-185-815-6

Query Match 46.4%; Score 32; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DPTTP 9
Db 5 DPTTP 9

RESULT 9
US-10-161-791-252
; Sequence 252, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-252

Query Match 46.4%; Score 32; DB 14; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDTPPL 10
| | | | |
DB 4 KMPRPPL 12

RESULT 10
US-10-116-275-52
Sequence 52, Application US/10116275
Publication No. US20030211476A1
GENERAL INFORMATION:
APPLICANT: Elan Pharmaceutical Technology
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Brayden, David
APPLICANT: Byrne, Daragh
APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance Up
OTHER INFORMATION: take Across the GIT"
US-10-116-275-52

Query Match 46.4%; Score 32; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DTPPP 9
| | | | |
DB 5 DTPPP 9

RESULT 11
US-10-611-440-188
Sequence 188, Application US/10611440
Publication No. US20040197912A1
GENERAL INFORMATION:
APPLICANT: Berinstein, Neil
APPLICANT: Gallichan, Scott
APPLICANT: Lovitt, Corey
APPLICANT: Farrington, Mark
APPLICANT: Pedyczak, Artur

APPLICANT: Radvanyi, Laszlo
APPLICANT: Singh-Sandhu, Devender
APPLICANT: Comen, Raymond P
APPLICANT: Cao, Shi-Xian
TITLE OF INVENTION: Tumor Antigens BFA4 and BCY1 for Prevention and/or Treatment of
TITLE OF INVENTION: Cancer
FILE REFERENCE: API-02-11-US
CURRENT APPLICATION NUMBER: US/10/611,440
CURRENT FILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: US 60/394,346
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/394,503
PRIOR FILING DATE: 2002-07-09
PRIOR APPLICATION NUMBER: US 60/411,833
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US 60/445,342
PRIOR FILING DATE: 2003-02-06
NUMBER OF SEQ ID NOS: 218
SOFTWARE: PatentIn version 3.2
SEQ ID NO 188
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: CLP-2825
US-10-611-440-188

Query Match 44.9%; Score 31; DB 16; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPLW 11
: : : : :
DB 2 ETSPLW 8

RESULT 12
US-10-437-708-168
Sequence 168, Application US/10437708
Publication No. US20040009555A1
GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/10/437,708
CURRENT FILING DATE: 2003-05-14
PRIOR APPLICATION NUMBER: US/09/547,693
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: PatentIn version 3.0
SEQ ID NO 168
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial/Unknown
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Synthetic
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
FEATURE:
NAME/KEY: SITE
LOCATION: (3)..(4)
OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-437-708-168

Query Match 43.5%; Score 30; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPL 10

```
Db          1 PTPPL 5
|||||
RESULT 13
US-10-418-032-168
; Sequence 168, Application US/10418032
; Publication No. US20050074838A1
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; FILE REFERENCE: OHU-0775
; CURRENT APPLICATION NUMBER: US/10/418,032
; PRIOR FILING DATE: 2003-04-16
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 168
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(4)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-418-032-168
Query Match          43.5%; Score 30; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 PTPPL 10
|||||
Db          1 PTPPL 5

RESULT 14
US-10-190-082-480
; Sequence 480, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Lasky, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P1905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 480
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-480
Query Match          43.5%; Score 30; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy          6 PTPPL 11
|||||
Db          1 PNPPRW 6

RESULT 15
US-10-437-708-165
; Sequence 165, Application US/10437708
; Publication No. US20040009555A1
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/10/437,708
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US/09/547,693
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 165
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)..(3)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)..(6)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-437-708-165
Query Match          43.5%; Score 30; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 PTPPL 10
|||||
Db          3 PTPPL 7

Search completed: May 26, 2005, 20:30:50
Job time : 155 secs
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OM protein - protein search, using sw model

Run on: May 26, 2005, 20:09:44 ; Search time 40 Seconds
(without alignments)
22.395 Million cell updates/sec

Title: US-10-047-945-4

Perfect score: 69

Sequence: 1 LKANDPTPLMI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 135920

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	78.3	10	1	US-08-657-163A-2
2	32	46.4	11	1	US-08-336-343A-31
3	32	46.4	11	3	US-08-652-877-31
4	32	46.4	11	3	US-08-476-515A-31
5	32	46.4	12	3	US-08-602-999A-252
6	32	46.4	12	4	US-09-500-124-252
7	30	43.5	6	3	US-09-232-446B-24
8	30	43.5	8	4	US-09-547-693-168
9	30	43.5	10	4	US-09-547-693-165
10	29	42.0	12	4	US-09-315-926A-18
11	28	40.6	10	3	US-09-133-341-7
12	28	40.6	10	4	US-09-739-852-7
13	27	39.1	6	1	US-07-989-290-2
14	27	39.1	6	1	US-08-271-698-2
15	27	39.1	6	1	US-08-468-596-2
16	27	39.1	6	4	US-09-295-996B-12
17	27	39.1	6	4	US-09-295-846B-15
18	27	39.1	6	4	US-09-551-737C-15
19	27	39.1	6	4	US-09-295-924B-2
20	27	39.1	6	4	US-09-551-738B-12
21	27	39.1	7	1	US-07-989-290-3
22	27	39.1	7	1	US-08-271-698-3
23	27	39.1	7	1	US-08-468-596-3
24	27	39.1	7	4	US-09-295-996B-13
25	27	39.1	7	4	US-09-295-846B-16
26	27	39.1	7	4	US-09-551-737C-16
27	27	39.1	7	4	US-09-295-924B-3

28	27	39.1	7	4	US-09-551-738B-13	Sequence 13, Appl
29	27	39.1	8	1	US-07-989-290-4	Sequence 4, Appl
30	27	39.1	8	1	US-08-271-698-4	Sequence 4, Appl
31	27	39.1	8	1	US-08-468-596-4	Sequence 4, Appl
32	27	39.1	8	4	US-09-295-996B-14	Sequence 14, Appl
33	27	39.1	8	4	US-09-295-846B-17	Sequence 17, Appl
34	27	39.1	8	4	US-09-551-737C-17	Sequence 17, Appl
35	27	39.1	8	4	US-09-295-924B-4	Sequence 4, Appl
36	27	39.1	8	4	US-09-551-738B-14	Sequence 14, Appl
37	27	39.1	10	4	US-09-295-996B-8	Sequence 8, Appl
38	27	39.1	10	4	US-09-295-846B-11	Sequence 11, Appl
39	27	39.1	10	4	US-09-551-737C-11	Sequence 11, Appl
40	27	39.1	10	4	US-09-295-924B-7	Sequence 7, Appl
41	27	39.1	10	4	US-09-551-738B-8	Sequence 8, Appl
42	27	39.1	11	1	US-09-393-941-3	Sequence 3, Appl
43	27	39.1	11	1	US-08-175-471-3	Sequence 3, Appl
44	27	39.1	11	2	US-08-429-054A-3	Sequence 3, Appl
45	27	39.1	11	2	US-08-718-777-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-657-163A-2
; Sequence 2, Application US/08657163A
; Patent No. 5744449
; GENERAL INFORMATION:
; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
; TITLE OF INVENTION: SYNTHETIC LTNFS AND THEIR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BINIE V. LIPPS
; STREET: 4509 MIMOSA DR.
; CITY: BELLAIRE
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
; SOFTWARE: MS WORD 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,163A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,340
; FILING DATE: 22 SEPTEMBER 1994
; CLASSIFICATION: 514
; APPLICATION NUMBER: 08/058,387
; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN R. CASPERSON
; REGISTRATION NUMBER: 28,198
; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-482-2961
; TELEFAX: 713-663-7290
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N

ORIGINAL SOURCE: SYNTHETIC
US-08-657-163A-2

Query Match 78.3%; Score 54; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.011; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
| | | | | | | | | |
DB 1 LKAMDPTPPL 10

RESULT 2

US-08-336-343A-31
Sequence 31, Application US/08336343A
Patent No. 5677144

GENERAL INFORMATION:

APPLICANT: Ullrich, Axel

APPLICANT: Alves, Frauke

TITLE OF INVENTION: CKK-2, A No. 5677144el Receptor Tyrosine Kinase

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/336,343A

FILING DATE: 08-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-065

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-336-343A-31

Query Match 46.4%; Score 32; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPPL 10
| | | | | | | | | |
DB 3 KMPPPRPPL 11

RESULT 3

US-08-652-877-31

Sequence 31, Application US/08652877

Patent No. 6187548

GENERAL INFORMATION:

APPLICANT: Akerstrom, Goran

APPLICANT: Uhlhlin, Claes

APPLICANT: Rask, Lars

APPLICANT: Crumley, Gregg R.

APPLICANT: Morse, Clarence C.

APPLICANT: Murray, Edward M.

APPLICANT: Hjaln, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd., 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355E-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3808
TELEFAX: 610-454-3816
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-652-877-31

Query Match 46.4%; Score 32; DB 3; Length 11;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPPL 10
| | | | | | | | | |
DB 3 KMPPPRPPL 11

RESULT 4

US-08-476-515A-31

Sequence 31, Application US/08476515A

Patent No. 6239270

GENERAL INFORMATION:

APPLICANT: Akerstrom, Goran

APPLICANT: Uhlhlin, Claes

APPLICANT: Rask, Lars

APPLICANT: Crumley, Gregg R.

APPLICANT: Morse, Clarence C.

APPLICANT: Murray, Edward M.

APPLICANT: Hjaln, Goran

TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

TITLE OF INVENTION: Thereof and DNA Encoding Same

NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:

ADDRESSEE: Martin Savitzky

STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
CITY: 3C43,
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Compaq PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 7.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,515A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00483
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9301764-8
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-476-515A-31

Query Match 46.4%; Score 32; DB 3; Length 11;
Best Local Similarity 66.7%; Pred. NO. 43;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KAMDPTPL 10
Db 3 KMPPPRPL 11

RESULT 5
US-08-602-999A-252
Sequence 252, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-252
Query Match 46.4%; Score 32; DB 3; Length 12;
Best Local Similarity 66.7%; Pred. NO. 47;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KAMDPTPL 10
Db 4 KMPPPRPL 12

RESULT 6
US-09-500-124-252
Sequence 252, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-252

Query Match 46.4%; Score 32; DB 4; Length 12;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPL 10
DB 4 KMPPRPPL 12

RESULT 7
US-09-232-446B-24

; Sequence 24, Application US/09232446B
; Patent No. 6228647
; GENERAL INFORMATION:
; APPLICANT: Voytas, Daniel F.
; APPLICANT: Gai, Xiaowu
; TITLE OF INVENTION: Transposable Element Protein that Directs DNA
; TITLE OF INVENTION: Integration to Specific Chromosomal Sites
; FILE REFERENCE: 2-98
; CURRENT APPLICATION NUMBER: US/09/232,446B
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 60/071,383
; PRIOR FILING DATE: 1998-01-15
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: mutant peptide
; OTHER INFORMATION: sequence
US-09-232-446B-24

Query Match 43.5%; Score 30; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 41e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPTPP 9
DB 1 LDPSPP 6

RESULT 8
US-09-547-693-168

; Sequence 168, Application US/09547693
; Patent No. 6639050
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; TITLE OF INVENTION: Glycoproteins
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/09/547,693
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 168
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc_feature

; OTHER INFORMATION: Synthetic
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; NAME/KEY: SITE
; LOCATION: (3)..(4)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-09-547-693-168

Query Match 43.5%; Score 30; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPL 10
DB 1 PTPPL 5

RESULT 9

US-09-547-693-165
; Sequence 165, Application US/09547693
; Patent No. 6639050
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; TITLE OF INVENTION: Glycoproteins
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/09/547,693
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 165
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; NAME/KEY: SITE
; LOCATION: (3)..(3)
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; NAME/KEY: SITE
; LOCATION: (5)..(6)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-09-547-693-165

Query Match 43.5%; Score 30; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPL 10
DB 3 PTPPL 7

RESULT 10

US-09-315-926A-18
; Sequence 18, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmut
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlingen, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/09/315,926A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3

; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: phage display peptide
US-09-315-926A-18

Query Match 42.0%; Score 29; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TPPLW 11
|||
Db 7 TPAW 11

RESULT 11
US-09-133-341-7
; Sequence 7, Application US/09133341A
; Patent No. 6162440
; GENERAL INFORMATION:
; APPLICANT: Hayward, Diane S.
; APPLICANT: Ling, Paul D.
; TITLE OF INVENTION: EBNA2 PEPTIDES AND METHODS OF USING SAME
; FILE REFERENCE: 87512
; CURRENT APPLICATION NUMBER: US/09/133,341A
; CURRENT FILING DATE: 1998-08-13
; EARLIER APPLICATION NUMBER: WO 97US2243
; EARLIER FILING DATE: 1997-02-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Virus Organism: Artificial
US-09-133-341-7

Query Match 40.6%; Score 28; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PTPPLW 11
|||
Db 2 PGPPW 7

RESULT 12
US-09-739-852-7
; Sequence 7, Application US/09739852
; Patent No. 6495144
; GENERAL INFORMATION:
; APPLICANT: Hayward, Diane S.
; APPLICANT: Ling, Paul D.
; TITLE OF INVENTION: EBNA2 PEPTIDES AND METHODS OF USING SAME
; FILE REFERENCE: 87512
; CURRENT APPLICATION NUMBER: US/09/739,852
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/133,341
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:

; OTHER INFORMATION: Description of Unknown Virus Organism: Artificial
US-09-739-852-7

Query Match 40.6%; Score 28; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PTPPLW 11
|||
Db 2 PGPPW 7

RESULT 13
US-07-989-290-2
; Sequence 2, Application US/07989290
; Patent No. 5358934
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Carlson, David A.
; TITLE OF INVENTION: Materials and Methods for Control
; TITLE OF INVENTION: of Pests
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,290
; FILING DATE: 19921211
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF/S&S-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-07-989-290-2

Query Match 39.1%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPP 9
|||
Db 2 DPAPP 6

RESULT 14
US-08-271-698-2
; Sequence 2, Application US/08271698
; Patent No. 5439821
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Carlson, David A.
; TITLE OF INVENTION: Materials and Methods for Control

;; TITLE OF INVENTION: of Pests
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: David R. Saliwanchik
;; STREET: 2421 N.W. 41st Street, Suite A-1
;; CITY: Gainesville
;; STATE: FL
;; COUNTRY: USA
;; ZIP: 32606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/271,698
;; FILING DATE: 07-JUL-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/989,290
;; FILING DATE: 11-DEC-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Saliwanchik, David R.
;; REGISTRATION NUMBER: 31,794
;; REFERENCE/DOCKET NUMBER: UF/S&S-127
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 904-375-8100
;; TELEFAX: 904-372-5800
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-271-698-2

Query Match 39.1%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTTP 9
Db 2 DPAPP 6

RESULT 15
US-08-468-596-2
;; Sequence 2, Application US/08468596
;; Patent No. 5629196
;; GENERAL INFORMATION:
;; APPLICANT: Borovsky, Dov
;; APPLICANT: Carlson, David A.
;; TITLE OF INVENTION: Materials and Methods for Control
;; TITLE OF INVENTION: of Pests
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: David R. Saliwanchik
;; STREET: 2421 N.W. 41st Street, Suite A-1
;; CITY: Gainesville
;; STATE: FL
;; COUNTRY: USA
;; ZIP: 32606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/468,596
;; FILING DATE: 06-JUN-1995

;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/271,698
;; FILING DATE: 07-JUL-1994
;; APPLICATION NUMBER: US/07/989,290
;; FILING DATE: 11-DEC-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Saliwanchik, David R.
;; REGISTRATION NUMBER: 31,794
;; REFERENCE/DOCKET NUMBER: UF/S&S-127
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 904-375-8100
;; TELEFAX: 904-372-5800
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-468-596-2

Query Match 39.1%; Score 27; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTTP 9
Db 2 DPAPP 6

Search completed: May 26, 2005, 20:19:10
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: May 26, 2005, 20:27:26 ; Search time 38 Seconds
(without alignments)
20.256 Million cell updates/sec

Title: US-10-047-945-7

Perfect score: 43

Sequence: 1 LKANDPTP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 606

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	46.5	5	2 B60274	major protein anti
2	18	41.9	4	2 I51049	metallothionein-A
3	18	41.9	8	2 S1919	alcohol dehydrogen
4	17	39.5	8	2 S21288	lectin - potato (f
5	13	30.2	6	2 P00008	angiotensin-conver
6	13	30.2	6	2 A19780	transferrin - bovi
7	13	30.2	6	2 P70709	T-cell receptor be
8	13	30.2	7	2 S12299	ICL2 protein - Par
9	13	30.2	8	2 S10783	enamelin f - bovin
10	13	30.2	8	2 J50317	leucokinin VII - M
11	13	30.2	8	2 I64832	Ca2+-transporting
12	13	27.9	3	3 I78890	tyrosine protein k
13	12	27.9	4	2 S33508	starvation-induced
14	12	27.9	4	2 S17255	ribosomal protein
15	12	27.9	5	1 HOROHA	proctolin - Americ
16	12	27.9	5	2 P50324	ribulose-bisphosph
17	12	27.9	5	2 A60411	proctolin - Atlant
18	12	27.9	6	2 A61049	halo-toxin - Pseud
19	12	27.9	6	2 I51317	bHLH transcription
20	12	27.9	7	2 A33098	244K exoantigen -
21	12	27.9	7	2 S09027	carboxylesterase (
22	12	27.9	7	2 I48086	DNA topoisomerase
23	12	27.9	7	2 S09066	globulin IV alpha
24	12	27.9	8	2 A33995	adipokinetic hormo
25	12	27.9	8	2 B44960	neuropeptide led-C
26	12	27.9	8	2 A58620	adipokinetic hormo
27	12	27.9	8	2 S55310	adipokinetic hormo
28	12	27.9	8	2 S10596	adipokinetic hormo
29	12	27.9	8	2 S08996	hypertrehalosemic

30 12 27.9 8 2 B49823 adipokinetic hormo
31 12 27.9 8 2 B39745 endoglycosylcerami
32 12 27.9 8 2 S16324 hypothetical prote
33 12 27.9 8 2 P70530 T-cell receptor be
34 12 27.9 8 2 S21273 cellulase (EC 3.2.
35 12 27.9 8 2 A23967 leucopyrokinin - M
36 12 27.9 8 2 A31570 angiotensin-conver
37 12 27.9 8 2 E60588 sperm-activating p
38 12 27.9 8 2 G05088 granulocyte-colony
39 12 27.9 8 4 I54017 granulocyte-colony
40 11 25.6 4 2 I57745 D-nannonate hydrol
41 11 25.6 5 2 A32516 cholecystokinin-5
42 11 25.6 5 2 B31836 20K protein - Rick
43 11 25.6 6 2 A46474 Fc epsilon RIIB -
44 11 25.6 6 4 S15596 orf 3 rara 5'-regi
45 11 25.6 7 2 S55548 mcrB protein - Esc

ALIGNMENTS

RESULT 1

B60274

major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)

C:Species: Mycobacterium tuberculosis

C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993

C:Accession: B60274

R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991

A>Title: Isolation and partial characterization of major protein antigens in the culture

A:Reference number: A60274; MUID:91099899; PMID:1898899

A:Accession: B60274

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-5 <NAG>

Query Match 46.5%; Score 20; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTP 8
Db 1 DPAP 4

RESULT 2

I51049

metallothionein-A - rainbow trout (fragment)

C:Species: Oncorhynchus mykiss (rainbow trout)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: I51049

R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.

Eur. J. Biochem. 230, 344-349, 1995

A>Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) me

A:Reference number: I51049; MUID:95324545; PMID:7601121

A:Accession: I51049

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-4 <OLS>

A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 41.9%; Score 18; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDP 6
Db 1 MDP 3

RESULT 3

S71919

alcohol dehydrogenase (EC 1.1.1.1) - grass carp (fragment)

C:Species: Ctenopharyngodon idella (grass carp)
 C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004
 C:Accession: S71919
 R:Tsuji, H.T.; Mock, W.Y.; Lau, K.K.; Fong, W.P.
 Biochim. Biophys. Acta 1296, 41-46, 1996
 A:Title: Proteolytic activation of grass carp (Ctenopharyngodon idellus) liver alcohol dehydrogenase
 A:Reference number: S71919; MUID:96350418; PMID:8765227
 A:Accession: S71919
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <TSU>
 A:Cross-references: UNIPROT:Q7LZ46
 A>Note: the source is designated Ctenopharyngodon idellus
 C:Keywords: NAD; oxidoreductase

Query Match 41.9%; Score 18; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPT 7
 |||
 Db 2 DPT 4

RESULT 4
 S21288
 lectin - potato (fragment)
 C:Species: Solanum tuberosum (potato)
 C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
 C:Accession: S21288
 R:Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
 Biochem. J. 283, 813-821, 1992
 A:Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization of a novel protein
 A:Reference number: S21288; MUID:92272683; PMID:1590771
 A:Accession: S21288
 A:Molecule type: protein
 A:Residues: 1-8 <MIL>
 A:Cross-references: UNIPROT:Q7M1V6
 A:Experimental source: var. Ulster Sceptre
 C:Function:
 A:Description: may be involved in defence mechanism of the plant
 C:Keywords: hydroxyproline; lectin

Query Match 39.5%; Score 17; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTP 8
 |||
 Db 2 ASTPSP 7

RESULT 5
 PQ0008
 angiotensin-converting enzyme inhibitor (FLP-1) - common fig
 N:Alternate names: ficus latex peptide 1
 C:Species: Ficus carica (common fig)
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
 C:Accession: PQ0008
 R:Maruyama, S.; Miyoshi, S.; Tanaka, H.
 Agric. Biol. Chem. 53, 2763-2767, 1989
 A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
 A:Reference number: PQ0008
 A:Accession: PQ0008
 A:Molecule type: protein
 A:Residues: 1-6 <MAR>
 A:Experimental source: latex
 C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 30.2%; Score 13; DB 2; Length 6;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

C:Species: Bos primigenius taurus (cattle)
 C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993
 C:Accession: A19780
 R:Brook, J.H.; Esparza, I.; Oliver, R.A.; Spooner, R.L.
 Biochem. Genet. 18, 851-860, 1980
 A:Title: Electrophoretic mobility of N- and C-terminal monoferric fragments of bovine transferrin - bovine (fragment)
 A:Reference number: A19780; MUID:81183891; PMID:7225082
 A:Accession: A19780
 A:Molecule type: protein
 A:Residues: 1-6 <BRO>

Query Match 30.2%; Score 13; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DP 6
 |||
 Db 1 DP 2

RESULT 7
 PT0709
 T-cell receptor beta chain V-D-J region (161-2K) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0709
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0709
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-6 <FEE>
 A:Experimental source: newborn thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 30.2%; Score 13; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DP 6
 |||
 Db 4 DP 5

RESULT 8
 S71299
 ICu2 protein - Paramecium tetraurelia (fragment)
 C:Species: Paramecium tetraurelia
 C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
 C:Accession: S71299
 R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
 Eur. J. Biochem. 238, 121-128, 1996
 A:Title: Characterization of centrin genes in Paramecium.
 A:Reference number: S71299; MUID:96248429; PMID:8665928
 A:Accession: S71299
 A:Molecule type: protein
 A:Residues: 1-7 <MAD>
 A:Experimental source: strain d4-2
 C:Genetics:
 A:Genetic code: SGC5

Query Match 30.2%; Score 13; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PTP 8
| |
Db 3 PPP 5

RESULT 9
S10783
enamelin f - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S10783
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albumin
A:Reference number: S10780; MUID:90336641; PMID:2379503
A:Accession: S10783
A:Molecule type: protein
A:Residues: 1-8 <STR>
C:Keywords: enamel; phosphoprotein

Query Match 30.2%; Score 13; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PTP 8
| |
Db 2 PLP 4

RESULT 10
JS0317
leucokinin VII - Madeira cockroach
C:Species: Leucophaea maderae (Madeira cockroach)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: JS0317
R:Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987
A:Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the first
A:Reference number: JS0317
A:Accession: JS0317
A:Molecule type: protein
A:Residues: 1-8 <HOL>
A:Cross-references: UNIPROT:P19989
C:Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile actin
C:Keywords: amidated carboxyl end; cephalomyotropic peptide
F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 30.2%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DP 6
| |
Db 1 DP 2

RESULT 11
I64832
Ca2+-transporting ATPase (EC 3.6.3.8) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I64832
R:Wu, K.
Am. J. Physiol. 264, 333-341, 1993
A:Title: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase in
A:Reference number: I51892
A:Accession: I64832
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-8 <RES>
A:Cross-references: UNIPROT:Q63139; GB:M99223; NID:g203644; PIDN:AAA40992.1; PID:g203646

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PTP 8
| |
Db 3 PPP 5

RESULT 9
S10783
enamelin f - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S10783
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albumin
A:Reference number: S10780; MUID:90336641; PMID:2379503
A:Accession: S10783
A:Molecule type: protein
A:Residues: 1-8 <STR>
C:Keywords: enamel; phosphoprotein

Query Match 30.2%; Score 13; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PTP 8
| |
Db 2 PLP 4

RESULT 10
JS0317
leucokinin VII - Madeira cockroach
C:Species: Leucophaea maderae (Madeira cockroach)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: JS0317
R:Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987
A:Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the first
A:Reference number: JS0317
A:Accession: JS0317
A:Molecule type: protein
A:Residues: 1-8 <HOL>
A:Cross-references: UNIPROT:P19989
C:Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile actin
C:Keywords: amidated carboxyl end; cephalomyotropic peptide
F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 30.2%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DP 6
| |
Db 1 DP 2

RESULT 11
I64832
Ca2+-transporting ATPase (EC 3.6.3.8) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I64832
R:Wu, K.
Am. J. Physiol. 264, 333-341, 1993
A:Title: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase in
A:Reference number: I51892
A:Accession: I64832
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-8 <RES>
A:Cross-references: UNIPROT:Q63139; GB:M99223; NID:g203644; PIDN:AAA40992.1; PID:g203646

C:Genetics:
A:Gene: SERCALB
C:Keywords: hydrolase

Query Match 30.2%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DP 6
| |
Db 1 DP 2

RESULT 12
I78890
tyrosine protein kinase - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: I78890
R:Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.
Oncogene 9, 3437-3448, 1994
A:Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine protein kinase
A:Reference number: I58407; MUID:95060800; PMID:7970703
A:Accession: I78890
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3 <RES>
A:Cross-references: GB:L33339; NID:g609536; PIDN:AAA64432.1; PID:g609538
C:Genetics:
A:Gene: p52ntk

Query Match 27.9%; Score 12; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PT 7
| |
Db 2 PT 3

RESULT 13
S53508
starvation-induced ribonuclease - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
C:Accession: S53508
R:Koeck, M.; Joefler, A.; Abel, S.; Glund, K.
Plant Mol. Biol. 27, 477-485, 1995
A:Title: cDNA structure and regulatory properties of a family of starvation-induced ribonucleases
A:Reference number: S53506; MUID:95201242; PMID:7894013
A:Accession: S53508
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <KOE>

Query Match 27.9%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PT 7
| |
Db 2 PT 3

RESULT 14
S17255
ribosomal protein Yml1, mitochondrial, questionable - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
A:Variety: strain 07173
C:Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
C:Accession: S17255
R:Grohmann, L.; Graack, H.R.; Kruff, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.
FEBS Lett. 284, 51-56, 1991

A:Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from
 A:Reference number: S17255; MUID:91285106; PMID:2060626

A:Accession: S17255
 A:Molecule type: protein

A:Residues: 1-4 <GRO>

A:Cross-references: UNIPROT:P36515

C:Comment: A coding region for this protein could not be identified in the genome of Sac

C:Genetics:

A:Genome: nuclear

C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 27.9%; Score 12; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TP 8

DB 3 TP 4

RESULT 15

HOROKA

proctolin - American cockroach

C:Species: Periplaneta americana (American cockroach)

C:Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004

C:Accession: A01644

R:Staratt, A.N.; Brown, B.E.

Life Sci. 17, 1253-1256, 1975

A:Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects

A:Reference number: A93048; MUID:76074708; PMID:576

A:Accession: A01644

A:Molecule type: protein

A:Residues: 1-5 <STA>

A:Cross-references: UNIPROT:P01373

A:Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmac

R:O'Shea, M.; Adams, M.E.

Science 213, 567-569, 1981

A:Title: Pentapeptide (proctolin) associated with an identified neuron.

A:Reference number: A94260; MUID:81225865; PMID:6113690

A:Contents: annotation; biological source

C:Comment: this peptide is found in the lateral white neurons, which occur (in the cockr

innervate the striated hindgut muscles in insects and stimulate contraction of these mus

C:Superfamily: proctolin

C:Keywords: neuropeptide

Query Match 27.9%; Score 12; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PT 7

DB 4 PT 5

Search completed: May 26, 2005, 20:37:01

Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 20:19:15 ; Search time 172 Seconds
(without alignments)
23.818 Million cell updates/sec

Title: US-10-047-945-7
Perfect score: 43
Sequence: 1 LKMDPTP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	41.9	8	Q6UA69	Q6ua69 carassius.c
2	18	41.9	8	Q7LZ46	Q7Lz46 ctenopharyn
3	17	39.5	8	Q6U7R2	Q6u7r2 cryptococcu
4	17	39.5	8	Q7M1V6	Q7m1v6 solanum tub
5	16	37.2	8	Q8BJ0	Q8bj0 bacterioph
6	16	37.2	8	Q8H9K1	Q8h9k1 bacterioph
7	15	34.9	8	Q94623	Q94623 manduca sex
8	15	34.9	8	Q99P40	Q99p40 mus musculu
9	14	32.6	6	1 SAPP SEPOF	P83569 sepia offic
10	14	32.6	8	1 LMT2 LOCM1	P22396 locusta mig
11	14	32.6	8	1 PK3 PERAM	P82687 periplaneta
12	14	32.6	8	1 RS7_MFCIT	P33564 mycobacteri
13	14	32.6	8	2 QY4J3	Q9y4j3 homo sapien
14	14	32.6	8	2 Q7IMR4	Q7imr4 brassica na
15	14	32.6	8	2 Q9TKS5	Q9tks5 leptospermu
16	14	32.6	8	2 Q9ET16	Q9et16 mesocricetu
17	14	32.6	8	2 Q9ET17	Q9et17 mus caroli
18	14	32.6	8	2 Q9ET18	Q9et18 mus spretus
19	14	32.6	8	2 Q9QVJ8	Q9qvj8 mus sp. nep
20	14	32.6	8	2 Q9RIU6	Q9riu6 mus musculu
21	13	30.2	6	1 TMOF SARBU	P41495 sarcophaga
22	13	30.2	7	1 ALL4_CARMA	P81807 carcinus ma
23	13	30.2	7	1 FAR1_HELTI	P41871 helisoma tr
24	13	30.2	7	1 UF04_MOUSE	P38642 mus musculu
25	13	30.2	7	2 Q15897	P35897 homo sapien
26	13	30.2	8	1 FAR1_PANRE	P41872 panagrellius
27	13	30.2	8	1 LCK1_LEUMA	P21140 leucophaea
28	13	30.2	8	1 LCK2_LEUMA	P21141 leucophaea
29	13	30.2	8	1 LCK7_LEUMA	P19989 leucophaea
30	13	30.2	8	2 Q9HCQ0	Q9hqc0 homo sapien
31	13	30.2	8	2 Q9N6M5	Q9n6m5 toxoplasma

32	13	30.2	8	2	Q9MD43	Q9md43 rattus norv
33	13	30.2	8	2	Q9R3X0	Q9r3x0 planktothri
34	13	30.2	8	2	Q9R7T2	Q9r7t2 escherichia
35	13	30.2	8	2	Q6LD23	Q6ld23 mus musculu
36	13	30.2	8	2	Q78ED1	Q78ed1 rattus norv
37	13	30.2	8	2	Q9WJ33	Q9wj33 suid herpes
38	12.5	29.1	8	2	Q6Y2F2	Q6y2f2 citruss sine
39	12	27.9	4	1	YLM1_YEAST	P36515 saccharomyc
40	12	27.9	5	1	PRCT_CARMA	P67857 carcinus ma
41	12	27.9	5	1	PRCT_LIMPO	P67858 limulus pol
42	12	27.9	5	1	PRCT_PERAM	P67859 periplaneta
43	12	27.9	8	1	ACI_THUAL	P18691 thunnus alb
44	12	27.9	8	1	AKH_LIBAU	P25418 libellula a
45	12	27.9	8	1	AKH_TABAT	P14595 tabanus atr

ALIGNMENTS

RESULT 1

ID Q6UA69 PRELIMINARY; PRT; 8 AA.
AC Q6UA69;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Metallothionein B (Metallothionein A) (Fragment).
OS Carassius cuvieri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=52617;
RN [1]
RP SEQUENCE FROM N.A.
RA He P., Xing J., Ren H.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY375240; AAQ83767.1; -;
DR EMBL; AY375239; AAQ83766.1; -;
FT NON TER 8
SQ SEQUENCE 8 AA; 882 MW; FA3DDEBAABA76AA6 CRC64;

Query Match 41.9%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDP 6
Db 1 MDP 3

RESULT 2

ID Q7LZ46 PRELIMINARY; PRT; 8 AA.
AC Q7LZ46;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP SEQUENCE.
RX MEDLINE=96350418; PubMed=8765227; DOI=10.1016/0167-4838(96)00051-9;
RA Tsui H.T., Mock W.Y., Lau K.K., Fong W.P.;
RT "Proteolytic activation of grass carp (Ctenopharyngodon idellus) liver
alcohol dehydrogenase";
RL Biochim. Biophys. Acta 1296:41-46(1996).
DR PIR; S71919; S71919.
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
FT NON TER 1

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FT NON_TER      8
SQ SEQUENCE      8 AA; 924 MW; DEA9D411B1B76AB5 CRC64;

Query Match      41.9%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 DPT 7
DB      2 DPT 4

RESULT 3
Q6U7R2
ID Q6U7R2 PRELIMINARY; PRT; 8 AA.
AC Q6U7R2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Squalene monooxygenase (EC 1.14.99.7) (Fragment).
GN Name=ERGI;
OS Cryptococcus neoformans var. grubii H99.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=235443;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H99;
RA Stuart L.T., Allen A., Dietrich F.S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV376718; RAQ8127.1; -.
DR GO; GO:0004506; F:squalene monooxygenase activity; IEA.
KW Monooxygenase; Oxidoreductase.
FT NON_TER      1
SQ SEQUENCE      8 AA; 811 MW; 0467776AAB1DD727 CRC64;

Query Match      39.5%; Score 17; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 LKAMPD 6
DB      1 LLAEDP 6

RESULT 4
Q7M1V6
ID Q7M1V6 PRELIMINARY; PRT; 8 AA.
AC Q7M1V6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lectin (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RA Millar D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R.,
RA Bolwell G.P.;
RT "Chitin-binding proteins in potato (Solanum tuberosum L.) tuber.
RT Characterization, immunolocalization and effects of wounding.";
RL Biochem. J. 283:813-821(1992).
DR PIR; S21288; S21288.
FT NON_TER      1
FT NON_TER      8
SQ SEQUENCE      8 AA; 771 MW; C37775A71B5BDDA CRC64;

Query Match      39.5%; Score 17; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      3 AMDPTP 8
DB      2 ASTPSP 7

RESULT 5
Q8SBJ0
ID Q8SBJ0 PRELIMINARY; PRT; 8 AA.
AC Q8SBJ0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Gp30.2 (Fragment).
GN Name=30.2;
OS Bacteriophage RB69.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=12353;
RN [1]
RP SEQUENCE FROM N.A.
RA Piesinien L., Kolesinskiene G., Truncaite L., Zajanckauskaite A.,
RA Nivinskas R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ439452; CAD28423.1; -.
FT NON_TER      8
SQ SEQUENCE      8 AA; 918 MW; F3B1A72041B76336 CRC64;

Query Match      37.2%; Score 16; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 MDPT 7
DB      1 MKPT 4

RESULT 6
Q8H9K1
ID Q8H9K1 PRELIMINARY; PRT; 8 AA.
AC Q8H9K1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Gp30.2 protein (Fragment).
GN Name=30.2;
OS Bacteriophage LZ10.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=192973;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolesinskiene G., Nivinskas R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ458400; CAD30256.1; -.
FT NON_TER      8
SQ SEQUENCE      8 AA; 918 MW; F3B1A72041B76336 CRC64;

Query Match      37.2%; Score 16; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 MDPT 7
DB      1 MKPT 4

RESULT 7
Q94623
ID Q94623 PRELIMINARY; PRT; 8 AA.
AC Q94623;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

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DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE MSUSP-2 protein (Fragment).
GN Name=usp;
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Spingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epidermis;
RX MEDLINE=97165493; PubMed=9013254;
RA Jindra M., Huang J.Y., Malone F., Ashina M., Riddiford L.M.;
RT "Identification and mRNA developmental profiles of two ultraspiracle
RL isoforms in the epidermis and wings of Manduca sexta.";
DR Insect Mol. Biol. 6:41-53(1997).
DR EMBL; U57921; AAB64235.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 892 MW; F165BB0415A76B16 CRC64;

Query Match 34.9%; Score 15; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDPT 7
Db 1 MEPS 4

RESULT 8
ID Q99P40 PRELIMINARY; PRT; 8 AA.
AC Q99P40;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE Repressor of GATA (Fragment).
GN Name=Rog;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57B6;
RX PubMed=14688323;
RA Miao S.-C., Kang B.Y., White I.A., Ho I.-C.;
RT "A repressor of GATA-mediated negative feedback mechanism of T cell
RT activation.";
RL J. Immunol. 172:170-177(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57B6;
RA Miao S.-C., Ho I.-C.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF355542; AAG59843.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 943 MW; FE3411B771B6C766 CRC64;

Query Match 34.9%; Score 15; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MDPTP 8
Db 1 MPQTP 5

RESULT 9
SAPP_SEPOF
ID SAPP_SEPOF STANDARD; PRT; 6 AA.
AC P83569;
DT 29-MAR-2004 (Rel. 43, Created)

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DT 29-MAR-2004 (Rel. 43, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sperm attracting peptide SepSAP.
OC Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY, AND
RP AMIDATION.
RC TISSUE=Egg;
RX MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;
RA Zatylny C., Marwin L., Gagnon J., Henry J.;
RT "Fertilization in Sepia officinalis: the first mollusk sperm-
RT attracting peptide.";
RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
CC -1- FUNCTION: Attracts sperm increasing the chances of gamete
CC collision.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: First appears in the ovarian follicles during
CC vitellogenesis. Accumulates in the oocytes before being secreted
CC during fertilization. Expression continues in the embedded oocyte.
CC Accumulates in the egg capsule after fertilization.
CC -1- MASS SPECTROMETRY: MW=596.6; METHOD=WALDI; RANGE=1-6; NOTE=Ref.1.
KW Amidation; Direct protein sequencing.
FT MOD RES 6 6 Valine amide.
SQ SEQUENCE 6 AA; 597 MW; 72C8676AA0470000 CRC64;

Query Match 32.6%; Score 14; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDP 6
Db 2 IDP 4

RESULT 10
LMT2 LOCM1
ID LMT2 LOCM1 STANDARD; PRT; 8 AA.
AC P22396;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Locustamyotropin 2 (LOM-MT-2).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin II, an
RT additional neuropeptide of Locusta migratoria. Member of the
RT cephalomyotropic peptide family.";
RL Insect Biochem. 20:479-484(1990).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SIMILARITY: Belongs to the pyrokinin family.
CC InterPro: IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Amidation; Direct protein sequencing; Neuropeptide; Pyrokinin.
FT MOD RES 8 8 Leucine amide.
SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;

Query Match 32.6%; Score 14; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTP 8

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Db          3 DFTP 6
PK3_PERAM  STANDARD;      PRT;      8 AA.
ID PK3_PERAM
AC P82687;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kinin-3 (Pea-K-3).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=98010462; PubMed=9350979; DOI=10.1016/S0167-0115(97)01029-X;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gade G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=907.92; METHOD=Electrospray; RANGE=1-8;
CC NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the kinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 8 8 Glycine amide.
SQ SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;

Query Match 32.6%; Score 14; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DFT 7
DB 1 DPS 3

RESULT 12
RS7_MYCIT STANDARD; PRT; 8 AA.
ID RS7_MYCIT
AC P33564;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 30S ribosomal protein S7 (Fragment).
GN Name=rpsG;
OS Mycobacterium intracellulare.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1767;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93197130; PubMed=84511173;
RA Nair J., Rouse D.A., Morris S.L.;
RT "Nucleotide sequence analysis of the ribosomal S12 gene of
RT Mycobacterium intracellulare.";
RL Nucleic Acids Res. 21:1039-1039(1993).
CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
CC directly to 16S rRNA where it nucleates assembly of the head
CC domain of the 30S subunit. Is located at the subunit interface
CC close to the decoding center, probably blocks exit of the E-site
CC rRNA (By similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
CC and S11 (By similarity).
CC -!- SIMILARITY: Belongs to the ribosomal protein S7P family.
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CC

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DR EMBL; L08171; AAA25376.1; -.
DR PIR; S35538; S35538.
DR HAMAP; MF_00480; -.
DR InterPro; IPR000235; Ribosomal_S7.
DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
KW Ribosomal protein; rRNA-binding; tRNA-binding; tRNA-binding.
FT INIT_MET 0 0 By similarity.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match 32.6%; Score 14; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTP 8
DB 5 PAP 7

RESULT 13
Q9Y4J3 PRELIMINARY; PRT; 8 AA.
ID Q9Y4J3
AC Q9Y4J3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Runt/68nt/MTG8 protein (Fragment).
GN Name=runt/68nt/MTG8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Bone marrow;
RX MEDLINE=95002916; PubMed=7919324;
RA Tighe J.E., Calabi E.;
RT "Alternative, out-of-frame runt/MTG8 transcripts are encoded by the
RT derivative (8) chromosome in the t(8;21) of acute myeloid leukemia
RT M2.";
RL Blood 84:2115-2121(1994).
DR EMBL; S74094; AAD14973.2; -.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 929 MW; 30B764405B17244B CRC64;

Query Match 32.6%; Score 14; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPT 7
DB 5 INPT 8

RESULT 14
Q7IMR4 PRELIMINARY; PRT; 8 AA.
ID Q7IMR4
AC Q7IMR4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ATP synthase beta subunit (fragment).
GN Name=atpB;
OS Brassica napus (Rape).
OG Chloroplast.

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Z.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF264734; AAF74768.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 919 MW; ECA1B1B764404406 CRC64;

Query Match 32.6%; Score 14; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDPT 7
 Db 3 INPT 6

RESULT 15

O9TKES PRELIMINARY; PRT; 8 AA.
 AC O9TKES;
 DT 01-MAY-2000 (TremBLrel. 13, Created)
 DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
 DE AtpB (Fragment).
 GN Name=atpB;
 OS Leptospermum erubescens.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Myrtaceae; Leptospermum.
 OX NCBI_TaxID=106049;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
 RL Aust. J. Bot. 48:621-628(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Healewood M., Quinn C.J.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF184690; AAF03860.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 876 MW; ECA1B1B764405056 CRC64;

Query Match 32.6%; Score 14; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDPT 7
 Db 3 INPT 6

Search completed: May 26, 2005, 20:36:15
 Job time : 176 secs

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OM protein - protein search, using sw model

Run on: May 26, 2005, 20:18:30 ; Search time 157 Seconds
(without alignments)
19.708 Million cell updates/sec

Title: US-10-047-945-7

Perfect score: 43

Sequence: 1 LKAWDPTP 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 160390

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	8	7	ABB80228
2	24	55.8	5	2	AAW53842
3	24	55.8	5	7	ABB80224
4	24	55.8	8	2	AAW45995
5	24	55.8	8	8	ADK10228
6	23	53.5	5	2	AAK37031
7	23	53.5	6	4	AAW68473
8	23	53.5	7	2	AAV50089
9	22	51.2	7	6	ABR82052
10	22	51.2	8	4	ADK01475
11	21	48.8	4	4	AAW74035
12	21	48.8	4	5	ABB81338
13	21	48.8	5	2	AAW24922
14	21	48.8	6	4	AAW74036
15	21	48.8	6	5	ABB81339
16	21	48.8	7	2	AAV40821
17	21	48.8	7	3	AAW17247
18	21	48.8	7	3	AAW17233
19	21	48.8	7	3	AAW17232
20	21	48.8	7	3	AAW30156
21	21	48.8	7	4	AAW46490
22	21	48.8	7	4	AAW46495
23	21	48.8	7	4	AAW45098
24	21	48.8	7	4	AAW44790
25	21	48.8	7	5	ABB73240

26	21	48.8	7	5	ABB73226	Abb73226	Src homol
27	21	48.8	7	5	ABB73225	Abb73225	Src homol
28	21	48.8	7	7	ADC44630	ADC44630	Endothel1
29	21	48.8	7	7	ADJ73394	ADJ73394	SH3 antag
30	21	48.8	7	7	ADJ73379	ADJ73379	SH3 antag
31	21	48.8	7	7	ADJ73380	ADJ73380	SH3 antag
32	21	48.8	7	8	ADJ53013	ADJ53013	CH1 delet
33	21	48.8	7	8	ADJ53014	ADJ53014	CH1 delet
34	21	48.8	7	8	ADJ53028	ADJ53028	CH1 delet
35	21	48.8	7	8	ADJ51974	ADJ51974	CH1 delet
36	21	48.8	7	8	ADJ51975	ADJ51975	CH1 delet
37	21	48.8	7	8	ADJ51989	ADJ51989	CH1 delet
38	21	48.8	7	8	ADQ08405	ADQ08405	IgG detec
39	21	48.8	7	8	ADQ08528	ADQ08528	IgG detec
40	21	48.8	7	8	ADQ28430	ADQ28430	IgG purif
41	21	48.8	7	8	ADQ28553	ADQ28553	IgG purif
42	21	48.8	7	8	ADQ07145	ADQ07145	IgG purif
43	21	48.8	7	8	ADQ07268	ADQ07268	IgG purif
44	21	48.8	8	4	ABP12619	ABP12619	HIV A02 B
45	21	48.8	8	4	ABP20550	ABP20550	HIV A03 m

ALIGNMENTS

RESULT 1

ABB80228
ID ABB80228 standard; peptide; 8 AA.

XX ABB80228;

DT 06-NOV-2003 (first entry)

DE Synthetic LTNP, LT-8.

XX Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW saliva; ELISA.

XX Synthetic.

OS WO2003060471-A2.

PN 24-JUL-2003.

PD 14-JAN-2003; 2003WO-US001044.

PP 14-JAN-2002; 2002US-00047945.

PR (LIPP/) LIPPS B V.

PA (LIPP/) LIPPS F W.

XX Lipps BV, Lipps FW;

XX WPI; 2003-636703/60.

XX Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT asthma or diabetes, by employing an ELISA on a saliva sample from a
PT patient.

XX Claim 7; Page 4; 24pp; English.

XX The sequences given in ABB80222-28 represent lethal toxin neutralising
CC factor (LTNP) peptides which may be used for reducing elevated levels of
CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
CC particular, the methods of the invention are useful for diagnosing and
CC treating conditions with elevated serum IGE levels, e.g. asthma,
CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid

CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 43; DB 7; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

QY 1 LKAMDPTP 8
 |||||
 Db 1 LKAMDPTP 8

RESULT 2

AAW53842
 ID AAW53842 standard; peptide; 5 AA.

XX AC AAW53842;

XX DT 08-JUL-1998 (first entry)

XX DE N-terminus of opossum LTNP.

XX KW LTNP, lethal toxin neutralising factor; opossum; envenomation; therapy;
 KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
 KW histamine reaction treatment.

XX OS Didelphis virginiana.

XX PN US5744449-A.

XX PD 28-APR-1998.

XX PF 03-JUN-1996; 96US-00657163.

XX PR 10-MAY-1993; 93US-00058387.

XX PR 22-SEP-1994; 94US-00310340.

XX PA (LIPP/) LIPPS B V.

XX PA (LIPP/) LIPPS F W.

XX PI Lipps FW, Lipps BV;

XX PS WPI; 1998-271108/24.

XX DR Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
 XX venom(s) from all major families of poisonous snakes.

XX PS Claim 5; Col 13; 11pp; English.

XX CC This sequence represents the peptide of the invention. It is a lethal
 CC Toxin Neutralising Factor (LTNP) moiety from a 68 kDa anti-haemorrhagic
 CC protein derived from an opossum. The peptide can be used in a method for
 CC treating a victim of envenomation from a poisonous snake, preferably a
 CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
 CC is useful for the treatment of snake bites, sepsis, allergies caused by
 CC the environment and treatment of bee or scorpion stings or toxicities
 CC caused by plant or bacterial toxins. The peptide can also be used in
 CC histamine reaction treatment. The peptide can be used in envenomation
 CC treatment for a variety of snakes without prior identification of the
 CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins

XX SQ

Sequence 5 AA;

Query Match 55.8%; Score 24; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
 |||||
 Db 1 LKAMD 5

RESULT 3

ABB80224
 ID ABB80224 standard; peptide; 5 AA.

XX AC ABB80224;

XX DT 06-NOV-2003 (first entry)

XX DE Synthetic LTNP, LT-5.

XX KW Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.

XX OS Synthetic.

XX PN WO2003060471-A2.

XX PD 24-JUL-2003.

XX PF 14-JAN-2003; 2003WO-US001044.

XX PR 14-JAN-2002; 2002US-00047945.

XX PA (LIPP/) LIPPS B V.

XX PA (LIPP/) LIPPS F W.

XX PI Lipps BV, Lipps FW;

XX PS WPI; 2003-636703/60.

XX PT Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

XX PS Disclosure; Page 3; 24pp; English.

XX CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX SQ Sequence 5 AA;

DE	Human papillomavirus peptide #2283.
XX	pathogenic virus; alternative reading frame; antigenic determinant;
KW	virucide; vaccine; therapeutic agent; infection; HPV.
KX	
OS	Human papillomavirus.
XX	
XX	WO2004011650-A2.
PN	
PD	05-FEB-2004.
XX	
XX	24-JUL-2003; 2003WO-EF008112.
PF	
XX	24-JUL-2002; 2002AT-00001124.
PR	
PR	11-JUL-2003; 2003EP-00450171.
XX	
PA	(INTE-) INTERCELL AG.
XX	
XX	Mattner F, Schmidt W, Habel A;
PI	
XX	WPI; 2004-169243/16.
DR	
XX	New polypeptide encoded by an alternative reading frame of a pathogenic
PT	virus comprising an antigenic determinant, useful for treating or
PT	preventing an infection with the pathogenic virus.
PT	
XX	
PS	Claim 18; Page 198; 220pp; English.
XX	
CC	This invention relates to a novel polypeptide encoded by an alternative
CC	reading frame of a pathogenic virus, where the polypeptide starts with a
CC	methionine amino acid residue, which comprises an antigenic determinant
CC	and more than 7 amino acid residues. The invention may be useful for the
CC	production of compounds with a virucide activity or the development of a
CC	vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC	agent. It is also useful for the manufacture of a medicament for treating
CC	or preventing an infection with the pathogenic virus. The present
CC	sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC	invention.
XX	
SQ	Sequence 8 AA;
Query Match	55.8%; Score 24; DB 8; Length 8;
Best Local Similarity	66.7%; Pred. No. 1.8e+06;
Matches	4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	3 AMDPTP 8 : 2 AVDPEP 7
DB	
RESULT 6	
AAR37031	ID AAR37031 standard; peptide; 5 AA.
XX	
AC	AAR37031;
XX	
DT	25-MAR-2003 (revised)
DT	28-JUL-1993 (first entry)
XX	
XX	Pentapeptide component #1 of N-linked glycoconjugate.
DE	beta-anomer; beta-glycosylamine linked glycoconjugate.
XX	
OS	Synthetic.
XX	
XX	EP538230-A1.
PN	
XX	21-APR-1993.
XX	
XX	14-OCT-1992; 92EP-00870165.
PF	
XX	15-OCT-1991; 91US-00776911.
PR	11-AUG-1992; 92US-00926786.

XX (MONS) MONSANTO CO.
 PA (OXFO-) OXFORD GLYCOSYSTEMS LTD.
 XX
 PI Dwek RA, Manger ID, Rademacher TW, Wong SYC;
 XX
 DR WPI; 1993-128045/16.
 XX
 XX N-linked peptide glyco-conjugate(s) prepn. - by reacting
 PT oligosaccharide(s) with ammonium bi:carbonate to maintain beta-anomeric
 PT configuration, and avoid sepn. of anomers.
 XX
 PS Claim 3; Page 32; 50pp; English.
 XX
 XX A peptide of 5-25 amino acid residues (pref. one of the pentapeptides
 CC AAR37031-3 or an atriopeptin e.g. atriopeptin A or D, see AAR37337-8)
 CC having an activated carboxyl group capable of forming a beta-
 CC glycosylamine linked glycoconjugate is reacted with an unprotected beta-
 CC glycosylamine deriv. of an oligosaccharide. The deriv. is prepared by
 CC reacting an unprotected oligosaccharide having up to 9 saccharide units
 CC with saturated ammonium bicarbonate at pH 8.0-8.5. The N-linked
 CC glycoconjugate is produced under conditions to directly maintain the beta
 CC -anomeric configuration. (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 5 AA;

Query Match 53.5%; Score 23; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. NO. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPT 7
 Db 1 MDPT 4
 |||||

RESULT 7
 AAB68473
 ID AAB68473 standard; peptide; 6 AA.
 XX
 AC AAB68473;
 XX
 DT 23-JUL-2001 (first entry)
 XX
 DE Mutated peptide derived from integrase of Ty5-6p, residues 1092-1097.
 XX
 KW Retrotransposon; polyprotein; integrase; Ty1-copia; silent chromatin;
 KW chromosomal integration; chromosomal targeting; Ty5; aging; oncogene.
 XX
 OS Synthetic.
 OS Saccharomyces paradoxus.
 XX
 PN US6228647-B1.
 XX
 PD 08-MAY-2001.
 XX
 PF 15-JAN-1999; 99US-00232446.
 XX
 PR 15-JAN-1998; 98US-0071383P.
 XX
 PA (IOWA) UNIV IOWA STATE RES FOUND INC.
 XX
 PI Voytas DF, Gai X;
 XX
 DR WPI; 2001-342676/36.
 XX
 PT Targeting integration of retrotransposon or retrovirus into silent
 PT chromatin by transforming a cell with modified integrase having a coding
 PT sequence for a peptide portion that interacts with chromatin at desired
 PT sites.
 XX
 PS Claim 13; Col 66; 41pp; English.
 XX

CC The present sequence represents a mutated portion of an integrase. The
 CC specification describes a method for targeting integration of
 CC retrotransposon of Ty1-copia group to desired location on a chromosome.
 CC The method uses a modified integrase in a retrotransposon, where the
 CC modified integrase contains a coding sequence for a peptide portion which
 CC specifically binds to protein bound to the chromosome or to particular
 CC nucleic acid sequences on chromosome. The method is useful for targeting
 CC integration of a retrotransposon of the Ty1-copia group to a desired
 CC location on a chromosome, especially into silent chromatin. The silent
 CC chromatin targeting of Ty5 is useful for tagging genes which are affected
 CC by aging and for studying oncogenes
 XX
 SQ Sequence 6 AA;

Query Match 53.5%; Score 23; DB 4; Length 6;
 Best Local Similarity 60.0%; Pred. NO. 1.8e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPT 8
 Db 1 LDPS 5
 :|||

RESULT 8
 AAY50089
 ID AAY50089 standard; peptide; 7 AA.
 XX
 AC AAY50089;
 XX
 DT 19-JAN-2000 (first entry)
 XX
 DE Coxsackievirus A VP1 conserved epitope 68.
 XX
 KW Virus; epitope; target; degenerate; PCR; primer; amplification; VP1;
 KW nonstructural protein 2A; conserved; base analogue; inosine;
 KW predetermined nucleotide; diagnosis; enterovirus; poliovirus.
 XX
 OS Synthetic.
 OS Coxsackievirus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2
 FT /label= Leu, Met
 XX
 PN W09953097-A2.
 XX
 PD 21-OCT-1999.
 XX
 PF 06-APR-1999; 99WO-US007513.
 XX
 PR 15-APR-1998; 98US-0081944P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Kilpatrick DR;
 XX
 DR WPI; 1999-620444/53.
 DR N-PSDB; AAZ32608.
 XX
 PT Designing degenerate polymerase chain reaction primers.
 XX
 PS Example 3; Page 18; 30pp; English.
 XX
 CC This sequence represents a conserved Coxsackievirus A (serotype A16) VP1
 CC epitope. The invention relates to a novel method for designing degenerate
 CC PCR primers (AAZ30975-231000, AAZ32601- AAZ32611) for amplifying target
 CC polynucleotides. This method comprises identifying uniquely conserved
 CC amino acid sequences (e.g, this epitope) in target proteins; synthesising
 CC degenerate polynucleotides encoding the conserved sequences; and
 CC substituting the synthesised polynucleotides with up to four
 CC predetermined nucleotides (e.g., inosine) at degenerate nucleotide
 CC positions. The nucleic acids comprise no more than 7 degenerate
 CC positions, have no more than 2 adjacent predetermined nucleotides and the

CC predetermined nucleotides are 3 bases away from the 3' end of the
 CC synthesised strand. The degenerate primers are useful for amplifying
 CC target polynucleotides by the polymerase chain reaction (PCR). The use of
 CC the method of designing degenerate primers useful for the detection of
 CC polioviruses in clinical samples is described in US585477. The degenerate
 CC primers facilitate PCR amplification of unknown polynucleotides, where
 CC the amino acid sequence encoded is known. The primers also allow for the
 CC correlation of the subsequent molecular based diagnosis with a
 CC serologically derived diagnosis

XX Sequence 7 AA;

Query Match 53.5%; Score 23; DB 2; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KAMDPTP 8
 | | | |
 Db 1 KXTDPPP 7

RESULT 9
 ABR82052

ID ABR82052 standard; peptide; 7 AA.

XX ABR82052;

XX 22-SEP-2003 (first entry)

XX N-terminal sequence from AMPK beta 1 (68-163) fusion protein SEQ ID:31.

XX AMP kinase beta subunit oligosaccharide binding domain; AMP kinase;
 KW oligosaccharide binding domain; enzyme; antidiabetic; gene therapy;
 KW antiarteriosclerotic; anorectic; cytostatic; diabetes; atherosclerosis;
 KW obesity; cancer; fusion protein.

XX Rattus rattus.

XX Synthetic.

XX WO2003056032-A1.

XX 10-JUL-2003.

XX 23-DEC-2002; 2002WO-AU001769.

XX 21-DEC-2001; 2001AU-00009728.

XX (SVIN-) ST VINCENTS INST MEDICAL RES.

XX Stapleton D, Kemp BE;

XX WPI; 2003-559281/52.

XX Screening for a compound that modulates the binding of an oligosaccharide
 PT to a beta subunit of AMP kinase by assessing the ability of the candidate
 PT compound to modulate binding of the polypeptide to the oligosaccharide.

XX Example; Page 33; 86pp; English.

XX The present invention describes a method of screening for a compound that
 CC modulates the binding of an oligosaccharide to a beta subunit of AMP
 CC kinase. The method comprises: (1) exposing a candidate compound to an
 CC oligosaccharide and a polypeptide comprising a beta subunit of AMP
 CC kinase, or its mutant and/or fragment that binds an oligosaccharide; and
 CC (2) assessing the ability of the candidate compound to modulate binding
 CC of the polypeptide to the oligosaccharide. An AMP kinase beta subunit
 CC oligosaccharide binding domain sequence has antidiabetic, cytostatic,
 CC antiarteriosclerotic and anorectic activities, and can be used in gene
 CC therapy. The method is useful for screening for a compound that modulates
 CC the binding of an oligosaccharide to a beta subunit of AMP kinase for
 CC treating or preventing a condition associated with AMP kinase activity
 CC e.g., diabetes, atherosclerosis, obesity or cancer. The present sequence
 CC represents an N-terminal sequence from AMPK beta 1 (68-163) fusion

CC protein, which is used in an example from the present invention
 XX Sequence 7 AA;

Query Match 51.2%; Score 22; DB 6; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AMDP 6
 | | | |
 Db 2 AMDP 5

RESULT 10
 ADK01475

ID ADK01475 standard; peptide; 8 AA.

XX ADK01475;

XX 06-MAY-2004 (first entry)

XX Hepatitis C virus 1b peptide SeqID127.

XX pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection.

XX Hepatitis C virus.

XX WO2004011650-A2.

XX 05-FEB-2004.

XX 24-JUL-2003; 2003WO-EP008112.

XX 24-JUL-2002; 2002AT-00001124.

XX 11-JUL-2003; 2003EP-00450171.

XX (INTE-) INTERCELL AG.

XX Mattner F, Schmidt W, Habel A;

XX WPI; 2004-169243/16.

XX New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.

XX Claim 7; SEQ ID NO 127; 220pp; English.

XX This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a hepatitis C virus peptide of the invention.

XX Sequence 8 AA;

Query Match 51.2%; Score 22; DB 8; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.8e+06;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
 : : : | | |
 Db 1 MRSPSPPT 8

RESULT 11
 AAB74035

ID AAB74035 standard; peptide; 4 AA.

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XX AC AAB74035;
XX DT 09-AUG-2001 (first entry)
XX DE Partial sequence contained in commercially available plasmid pMBac.
XX KW VEGF/PDGF-like factor; vascular endothelial growth factor; VEGF;
XX KW platelet derived growth factor; PDGF; neovascularisation; disease.
XX OS Synthetic.
XX PN JP2001017188-A.
XX PD 23-JAN-2001.
XX PF 24-APR-2000; 2000JP-00122994.
XX PR 22-APR-1999; 99JP-00115516.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PA (HERI-) HERIKKUSU KENKYUSHO KK.
XX DR WPI; 2001-285410/30.
XX PT New VEGF/PDGF-like factor useful for the development of treating agents
XX PT for diseases accompanied by accentuation of abnormal neovascularization.
XX PS Disclosure; Page 46; 52pp; Japanese.
XX CC The present sequence is provided in a specification relating to
CC a novel vascular endothelial growth factor (VEGF)/platelet derived growth
CC factor (PDGF)-like factor of 345 amino acids, or to a sequence in which
CC at least one amino acid is deleted, replaced or added compared to the
CC native sequence. The nucleotide sequence encoding the VEGF/PDGF-like
CC factor may be integrated into a vector and used to transform a host cell.
CC The VEGF/PDGF-like factor may be used in the development of agents for
CC treating diseases associated with abnormal neovascularisation
XX SQ Sequence 4 AA;

Query Match 48.8%; Score 21; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPTP 8
DB 1 DPSP 4

RESULT 12
ABB81338
ID ABB81338 standard; peptide; 4 AA.
XX AC ABB81338;
XX DT 23-AUG-2002 (first entry)
XX DE Human VPLF related peptide sequence SEQ ID NO:34.
XX KW Human; VPLF; VEGF/PDGF-like factor; vascular endothelial growth factor;
XX KW platelet-derived growth factor; antibody; inhibition; growth factor;
XX KW vasotrophic; vulnary; nephrotropic; cardiant; antidiabetic; antianaemic;
XX KW antiatherosclerotic; osteopathic; antirheumatic; antiarthritic;
XX KW antipsoriatic; arthritis; ischaemic disease; wound healing.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200233094-A1.
XX PD 25-APR-2002.
XX PT

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PF 19-OCT-2001; 2001WO-JP009218.
XX PR 19-OCT-2000; 2000JP-00319985.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PA (HELI-) HELIX RES INST.
XX PI Shitara K, Furuya A;
XX WPI; 2002-394558/42.
XX DR
XX PT Antibody specifically recognizing VPLF or its variant and inhibiting its
XX PT activity, applicable in diagnostics and remedies for VPLF-participating
XX PT diseases like arthritis, ischemic diseases and retarded wound healing.
XX PS Example; Page 59; 136pp; Japanese.
XX CC The present invention describes an antibody which specifically recognises
XX CC the human VPLF (vascular endothelial growth factor (VEGF)/platelet-
XX CC derived growth factor (PDGF-like factor) protein, and inhibits the
XX CC activity of this protein as a growth factor. The antibody has vasotropic,
XX CC vulnary, nephrotropic, cardiant, antidiabetic, antiatherosclerotic,
XX CC antianaemic, osteopathic, antirheumatic, antiarthritic and antipsoriatic
XX CC activities. The antibody is applicable in diagnostics and remedies for
XX CC VPLF-participated diseases like arthritis, ischaemic diseases and
XX CC retarded wound healing. The present sequence represents a human VPLF
XX CC related peptide sequence, which is used in an example from the present
XX CC invention
XX SQ Sequence 4 AA;

Query Match 48.8%; Score 21; DB 5; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPTP 8
DB 1 DPSP 4

RESULT 13
AAW24922
ID AAW24922 standard; peptide; 5 AA.
XX AC AAW24922;
XX DT 25-MAR-2003 (revised)
XX DT 17-OCT-1997 (first entry)
XX DE Vesicular stomatitis virus nucleocapsid protein #2.
XX KW Etiological agent; autoimmune disease; systemic lupus erythematosus; SLE;
XX KW Ro/SSA; immunoreactive; autoantibody; antigenicity; nucleocapsid;
XX KW vesicular stomatitis virus.
XX OS Vesicular stomatitis virus.
XX PN US5637454-A.
XX PD 10-JUN-1997.
XX PF 07-NOV-1994; 94US-00335198.
XX PR 31-JAN-1990; 90US-00472947.
XX PR 31-JAN-1991; 91US-00648205.
XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX PI Harley JB;
XX WPI; 1997-319066/29.
XX PT Determination of immunogenic agent in auto-immune disease - by

```

identifying protein sequences homologous to self-antigen sequences.

Example 2; Col 17; 36pp; English.

The invention relates to methods to determine the etiological agent of autoimmune diseases such as systemic lupus erythematosus (SLE). A common antigen for SLE and closely related disorders is the 60 kD protein-RNA particle: Ro/SSA, present in all cells studied to date. Staphylococcus V8 protease digestion of this protein reveals bands of 51, 40, 35, 28 and 13 kD which are strongly immunoreactive with SLE autoantibodies. From the 13 kD band, peptide AAW24911 demonstrated maximal antigenicity against anti-Ro/SSA autoantibodies. Peptides immunoreactive with SLE autoantibodies can then be used to screen for other peptides reactive with the antibodies. An example of such a peptide is the sequence presented here which is derived from the nucleocapsid protein of the Indiana serotype of the vesicular stomatitis virus. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 5 AA;

Query Match 48.8%; Score 21; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
| | | | |
DB 1 LKALD 5

RESULT 14
AAB74036
ID AAB74036 standard; peptide; 6 AA.
AC AAB74036;
AD
AE
AF 09-AUG-2001 (first entry)
AG
AH Synthetic protein #1 N-terminal sequence.
AI VEGF/PDGF-like factor; vascular endothelial growth factor; VEGF;
AJ platelet derived growth factor; PDGF; neovascularisation; disease.
AK Synthetic.
AL JP2001017188-A.
AM
AN 23-JAN-2001.
AO 24-APR-2000; 2000JP-00122994.
AP
AQ 22-APR-1999; 99JP-00115516.
AR (KYOW) KYOWA HAKKO KOGYO KK.
AS (HERI-) HERIKKUSU KENKYUSHO KK.
AT WPI; 2001-285410/30.
AU New VEGF/PDGF-like factor useful for the development of treating agents
AV for diseases accompanied by accentuation of abnormal neovascularization.
AW Disclosure; Page 46; 52pp; Japanese.
AX The present sequence is provided in a specification relating to
AY a novel vascular endothelial growth factor (VEGF)/platelet derived growth
AZ factor (PDGF)-like factor of 345 amino acids, or to a sequence in which
BA at least one amino acid is deleted, replaced or added compared to the
BB native sequence. The nucleotide sequence encoding the VEGF/PDGF-like
BC factor may be integrated into a vector and used to transform a host cell.
BD The VEGF/PDGF-like factor may be used in the development of agents for
BE treating diseases associated with abnormal neovascularisation. The
BF present sequence is the N-terminal sequence of the protein shown in
BG AAB74033

SQ Sequence 6 AA;

Query Match 48.8%; Score 21; DB 4; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPTP 8
| | | | |
DB 1 DPSP 4

RESULT 15
ABB81339
ID ABB81339 standard; peptide; 6 AA.
AC ABB81339;
AD
AE 23-AUG-2002 (first entry)
AF Human VPLF related peptide sequence SEQ ID NO:35.
AG Human; VPLF; VEGF/PDGF-like factor; vascular endothelial growth factor;
AH platelet-derived growth factor; antibody; inhibition; growth factor;
AI vasotrophic; vulnery; nephrotropic; cardiant; antidiabetic; antianaemic;
AJ antiarteriosclerotic; osteopathic; antirheumatic; antiarthritic;
AK antipsoriatic; arthritis; ischaemic disease; wound healing.
AL Homo sapiens.
AM Synthetic.
AN WO200233094-A1.
AO 25-APR-2002.
AP 19-OCT-2001; 2001WO-JP009218.
AQ 19-OCT-2000; 2000JP-00319985.
AR (KYOW) KYOWA HAKKO KOGYO KK.
AS (HELI-) HELIX RES INST.
AT Shitara K, Furuya A;
AU WPI; 2002-394558/42.
AV Antibody specifically recognizing VPLF or its variant and inhibiting its
AW activity, applicable in diagnostics and remedies for VPLF-participating
AX diseases like arthritis, ischemic diseases and retarded wound healing.
AY Example; Page 62; 136pp; Japanese.
AZ The present invention describes an antibody which specifically recognises
BA the human VPLF (vascular endothelial growth factor (VEGF)/platelet-
BB derived growth factor (PDGF-like factor) protein, and inhibits the
BC activity of this protein as a growth factor. The antibody has vasotropic,
BD vulnery, nephrotropic, cardiant, antidiabetic, antiarteriosclerotic,
BE antianaemic, osteopathic, antirheumatic, antiarthritic and antipsoriatic
BF activities. The antibody is applicable in diagnostics and remedies for
BG VPLF-participated diseases like arthritis, ischaemic diseases and
BH retarded wound healing. The present sequence represents a human VPLF
BI related peptide sequence, which is used in an example from the present
BJ invention
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Job time : 164 secs

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OM protein - protein search, using sw model

Run on: May 26, 2005, 20:36:28 ; Search time 133 Seconds
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20.750 Million cell updates/sec

Title: US-10-047-945-7
Perfect score: 43
Sequence: 1 LKAMDPTP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 83607

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:**

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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	24	55.8	5	14 US-10-047-945-3	Sequence 3, Appli
3	24	55.8	8	9 US-09-758-128-20	Sequence 20, Appli
4	24	55.8	8	9 US-09-758-128-23	Sequence 23, Appli
5	24	55.8	8	9 US-09-758-128-26	Sequence 26, Appli
6	24	55.8	8	9 US-09-758-128-29	Sequence 29, Appli
7	24	55.8	8	9 US-09-758-426-20	Sequence 20, Appli
8	24	55.8	8	9 US-09-758-426-23	Sequence 23, Appli
9	24	55.8	8	9 US-09-758-426-26	Sequence 26, Appli
10	24	55.8	8	9 US-09-758-426-29	Sequence 29, Appli
11	24	55.8	8	9 US-09-758-198-20	Sequence 20, Appli
12	24	55.8	8	9 US-09-758-198-23	Sequence 23, Appli
13	24	55.8	8	9 US-09-758-198-26	Sequence 26, Appli

14	24	55.8	8	9	US-09-758-138-29	Sequence 29, Appli
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16	24	55.8	8	10	US-09-861-661-23	Sequence 23, Appli
17	24	55.8	8	10	US-09-861-661-26	Sequence 26, Appli
18	24	55.8	8	10	US-09-861-661-29	Sequence 29, Appli
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39	21	48.8	7	15	US-10-653-048-289	Sequence 289, Appli
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44	21	48.8	8	15	US-10-149-138-1937	Sequence 1937, Appli
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ALIGNMENTS

RESULT 1
US-10-047-945-7
; Sequence 7, Application US/10047945
; Publication No. US2003015755A1
; GENERAL INFORMATION:
; APPLICANT: LIPES, BINTIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IGE)IMPLICATED DISORDERS
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
US-10-047-945-7

Query Match 100.0%; Score 43; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8

Db 1 LKAMDPTP 8

RESULT 2

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US-10-047-945-3
; Sequence 3, Application US/10047945
; Publication No. US2003015755A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (Ige)IMPLICATED DISORDERS
; FILE REFERENCE: FWPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
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; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-3

Query Match          55.8%; Score 24; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
Db 1 LKAMD 5

RESULT 3
US-09-758-128-20
; Sequence 20, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: PRT
; ORGANISM: Bovine
US-09-758-128-20

Query Match          55.8%; Score 24; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AMDPTP 8
Db 1 AISPTP 6

RESULT 4
US-09-758-128-23
; Sequence 23, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
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; TYPE: PRT
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QY 3 AMDPTP 8
Db 1 AISPTP 6

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; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
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; TYPE: PRT
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US-09-758-128-26

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Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AMDPTP 8
Db 1 AISPTP 6

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; Sequence 29, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
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; TYPE: PRT
; ORGANISM: Mouse
US-09-758-128-29

Query Match          55.8%; Score 24; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AMDPTP 8
Db 1 AISPTP 6
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;; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
;; FILE REFERENCE: 016786/0214
;; CURRENT APPLICATION NUMBER: US/09/758,128
;; CURRENT FILING DATE: 2001-01-12
;; PRIOR APPLICATION NUMBER: 09/194,218
;; PRIOR FILING DATE: 1999-02-05
;; PRIOR APPLICATION NUMBER: AU PN9990
;; PRIOR FILING DATE: 1996-05-22
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 29
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Rat
US-09-758-128-29

Query Match 55.8%; Score 24; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AMDPTP 8
|: |||
Db 1 AISPTP 6

RESULT 7
US-09-758-426-20
; Sequence 20, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020169116A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Bovine
US-09-758-426-20

Query Match 55.8%; Score 24; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AMDPTP 8
|: |||
Db 1 AISPTP 6

RESULT 8
US-09-758-426-23
; Sequence 23, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020169116A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218

;; PRIOR FILING DATE: 1999-02-05
;; PRIOR APPLICATION NUMBER: AU PN9990
;; PRIOR FILING DATE: 1996-05-22
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 23
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Porcine
US-09-758-426-23

Query Match 55.8%; Score 24; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AMDPTP 8
|: |||
Db 1 AISPTP 6

RESULT 9
US-09-758-426-26
; Sequence 26, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020169116A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mouse
US-09-758-426-26

Query Match 55.8%; Score 24; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AMDPTP 8
|: |||
Db 1 AISPTP 6

RESULT 10
US-09-758-426-29
; Sequence 29, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020169116A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0

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/ SEQ ID NO 29
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Rat
US-09-758-426-29

Query Match          55.8%; Score 24; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 AMDPTP 8
       |: |||
Db      1 AISPTP 6

RESULT 11
US-09-758-198-20
/ Sequence 20, Application US/09758198
/ Publication No. US20020187925A1
/ GENERAL INFORMATION:
/ APPLICANT: KINGSTON, David J.
/ APPLICANT: GERRATY, No. US20020187925A1man L.
/ APPLICANT: WESTERBOOK, Simon L.
/ TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
/ TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
/ FILE REFERENCE: 016786/0214
/ CURRENT APPLICATION NUMBER: US/09/758,198
/ CURRENT FILING DATE: 2001-01-12
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
/ PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 20
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Bovine
US-09-758-198-20

Query Match          55.8%; Score 24; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 AMDPTP 8
       |: |||
Db      1 AISPTP 6

RESULT 12
US-09-758-198-23
/ Sequence 23, Application US/09758198
/ Publication No. US20020187925A1
/ GENERAL INFORMATION:
/ APPLICANT: KINGSTON, David J.
/ APPLICANT: GERRATY, No. US20020187925A1man L.
/ APPLICANT: WESTERBOOK, Simon L.
/ TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
/ TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
/ FILE REFERENCE: 016786/0214
/ CURRENT APPLICATION NUMBER: US/09/758,198
/ CURRENT FILING DATE: 2001-01-12
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
/ PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 23
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/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Porcine
US-09-758-198-23

Query Match          55.8%; Score 24; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 AMDPTP 8
       |: |||
Db      1 AISPTP 6

RESULT 13
US-09-758-198-26
/ Sequence 26, Application US/09758198
/ Publication No. US20020187925A1
/ GENERAL INFORMATION:
/ APPLICANT: KINGSTON, David J.
/ APPLICANT: GERRATY, No. US20020187925A1man L.
/ APPLICANT: WESTERBOOK, Simon L.
/ TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
/ TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
/ FILE REFERENCE: 016786/0214
/ CURRENT APPLICATION NUMBER: US/09/758,198
/ CURRENT FILING DATE: 2001-01-12
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
/ PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 26
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Mouse
US-09-758-198-26

Query Match          55.8%; Score 24; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 AMDPTP 8
       |: |||
Db      1 AISPTP 6

RESULT 14
US-09-758-198-29
/ Sequence 29, Application US/09758198
/ Publication No. US20020187925A1
/ GENERAL INFORMATION:
/ APPLICANT: KINGSTON, David J.
/ APPLICANT: GERRATY, No. US20020187925A1man L.
/ APPLICANT: WESTERBOOK, Simon L.
/ TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
/ TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
/ FILE REFERENCE: 016786/0214
/ CURRENT APPLICATION NUMBER: US/09/758,198
/ CURRENT FILING DATE: 2001-01-12
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
/ PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 29
/ LENGTH: 8
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; TYPE: PRT
; ORGANISM: Rat
US-09-758-198-29

Query Match 55.8%; Score 24; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AMDPTP 8
|: |||
Db 1 AISPTP 6

RESULT 15

US-09-861-661-20
; Sequence 20, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Bos sp.
US-09-861-661-20

Query Match 55.8%; Score 24; DB 10; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AMDPTP 8
|: |||
Db 1 AISPTP 6

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Job time : 157 secs

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OM protein - protein search, using sw model

Run on: May 26, 2005, 20:30:57 ; Search time 40 Seconds
(without alignments)
14,930 Million cell updates/sec

Title: US-10-047-945-7

Perfect score: 43

Sequence: 1 LKANDPTP 8

Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	24	55.8	5	1	US-08-657-163A-3
2	23	53.5	5	1	US-07-926-786-1
3	23	53.5	6	3	US-09-232-446B-24
4	23	53.5	7	3	US-09-147-933-35
5	22	51.2	7	2	US-08-666-473-60
6	21	48.8	5	1	US-07-657-769B-1
7	21	48.8	5	1	US-07-657-769B-23
8	21	48.8	5	1	US-07-657-769B-62
9	21	48.8	5	1	US-08-335-198-20
10	21	48.8	5	1	US-07-789-184-68
11	21	48.8	5	1	US-08-475-263-68
12	21	48.8	5	1	US-08-485-886-68
13	21	48.8	5	2	US-08-477-362-68
14	21	48.8	5	2	US-08-477-134-68
15	21	48.8	5	3	US-08-473-489A-68
16	21	48.8	5	3	US-08-485-695-68
17	21	48.8	5	3	US-08-018-760-68
18	21	48.8	7	2	US-08-666-473-39
19	21	48.8	7	4	US-09-295-316-4
20	21	48.8	7	4	US-09-428-082B-288
21	21	48.8	7	4	US-09-428-082B-289
22	21	48.8	7	4	US-09-428-082B-303
23	21	48.8	8	1	US-07-789-184-190
24	21	48.8	8	1	US-08-475-263-190
25	21	48.8	8	1	US-08-485-886-190
26	21	48.8	8	2	US-08-477-362-190
27	21	48.8	8	2	US-08-477-134-190

28 21 48.8 8 3 US-08-473-489A-190 Sequence 190, Appl
29 21 48.8 8 3 US-08-485-695-190 Sequence 190, Appl
30 21 48.8 8 3 US-08-018-760-190 Sequence 190, Appl
31 20 46.5 5 1 US-07-657-769B-25 Sequence 25, Appl
32 20 46.5 5 1 US-07-657-769B-27 Sequence 27, Appl
33 20 46.5 5 1 US-07-657-769B-64 Sequence 64, Appl
34 20 46.5 5 1 US-07-657-769B-66 Sequence 66, Appl
35 20 46.5 5 1 US-07-989-290-1 Sequence 1, Appl
36 20 46.5 5 1 US-08-271-698-1 Sequence 1, Appl
37 20 46.5 5 1 US-08-468-596-1 Sequence 1, Appl
38 20 46.5 5 1 US-07-789-184-70 Sequence 70, Appl
39 20 46.5 5 1 US-07-789-184-72 Sequence 72, Appl
40 20 46.5 5 1 US-08-460-343B-46 Sequence 46, Appl
41 20 46.5 5 1 US-08-475-263-70 Sequence 70, Appl
42 20 46.5 5 1 US-08-475-263-72 Sequence 72, Appl
43 20 46.5 5 1 US-08-398-028B-46 Sequence 46, Appl
44 20 46.5 5 1 US-08-485-886-70 Sequence 70, Appl
45 20 46.5 5 1 US-08-485-886-72 Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-08-657-163A-3
; Sequence 3, Application US/08657163A
; Patent No. 5744449
; GENERAL INFORMATION:
; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
; TITLE OF INVENTION: SYNTHETIC LTNFS AND THEIR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BINIE V. LIPPS
; STREET: 4509 MIMOSA DR.
; CITY: BELLAIRE
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
; SOFTWARE: MS WORD 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,163A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,340
; FILING DATE: 22 SEPTEMBER 1994
; CLASSIFICATION: 514
; APPLICATION NUMBER: 08/058,387
; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN R. CASPERSON
; REGISTRATION NUMBER: 28,198
; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-482-2961
; TELEFAX: 713-663-7290
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 3
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: N

ORIGINAL SOURCE: SYNTHETIC
US-08-657-163A-3

Query Match 55.8%; Score 24; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
|||
Db 1 LKAMD 5

RESULT 2

US-07-926-786-1
; Sequence 1, Application US/07926786
; Patent No. 5280113
; GENERAL INFORMATION:
; APPLICANT: Rademacher, Thomas W.
; APPLICANT: Manger, Ian D.
; APPLICANT: Wong, Simon
; APPLICANT: Dwek, Raymond A.
; TITLE OF INVENTION: Method for Producing Synthetic N-Linked
; TITLE OF INVENTION: Glycoconjugates
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/926,786
; FILING DATE: 19920811
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/776911
; FILING DATE: 15-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/394691
; FILING DATE: 16-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-27(904)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-926-786-1

Query Match 53.5%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPT 7
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Db 1 MDPT 4

RESULT 3

US-09-232-446B-24
; Sequence 24, Application US/09232446B

; Patent No. 6228647
; GENERAL INFORMATION:
; APPLICANT: Voytas, Daniel F.
; APPLICANT: Gai, Xiaowu
; TITLE OF INVENTION: Transposable Element Protein that Directs DNA
; TITLE OF INVENTION: Integration to Specific Chromosomal Sites
; FILE REFERENCE: 2-98
; CURRENT APPLICATION NUMBER: US/09/232,446B
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 60/071,383
; PRIOR FILING DATE: 1998-01-15
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mutant peptide
; OTHER INFORMATION: sequence
US-09-232-446B-24

Query Match 53.5%; Score 23; DB 3; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPT 8
:|:|:
Db 1 LDPSP 5

RESULT 4

US-09-147-933-35
; Sequence 35, Application US/09147933A
; Patent No. 6168917
; GENERAL INFORMATION:
; APPLICANT: Kilpatrick, David
; TITLE OF INVENTION: DETECTION AND IDENTIFICATION OF
; TITLE OF INVENTION: NON-POLIO ENTEROVIRUSES
; FILE REFERENCE: 62242/US
; CURRENT APPLICATION NUMBER: US/09/147,933A
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: PCT/US97/17734
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: U. S. 60/027,353
; EARLIER FILING DATE: 1996-10-02
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: "RESIDUE 2 = LEU OR MET"
; OTHER INFORMATION: peptide
US-09-147-933-35

Query Match 53.5%; Score 23; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDTP 8
|:|:|
Db 1 KXTDPPP 7

RESULT 5

US-08-666-473-60
; Sequence 60, Application US/08666473
; Patent No. 5843713
; GENERAL INFORMATION:

;; APPLICANT: YOSHIDA, Atsuo
;; APPLICANT: TAKEUCHI, Makoto
;; TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
;; TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
;; TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN
;; NUMBER OF SEQUENCES: 114
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/666,473
;; FILING DATE: 19-SEP-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/JP95/02238
;; FILING DATE: 01-NOV-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 7-22101
;; FILING DATE: 09-FEB-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 6-269111
;; FILING DATE: 01-NOV-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 16887/837
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 60:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-666-473-60

Query Match 51.2%; Score 22; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AMDPTP 8
Db 2 AMTAP 7

RESULT 6
US-07-657-769B-1
; Sequence 1, Application US/07657769B
; Patent No. 5256766
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IRELL & MANELLA
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/657,769B
;; FILING DATE: 19910219
;; CLASSIFICATION: 435
;; NAME: MURASHIGE, KATE H.
;; REGISTRATION NUMBER: 29,959
;; REFERENCE/DOCKET NUMBER: 2000-0502:00
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-327-7250
;; TELEFAX: 415-327-2951
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-07-657-769B-1

Query Match 48.8%; Score 21; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDPTP 8
Db 1 LDPRP 5

RESULT 7
US-07-657-769B-23
; Sequence 23, Application US/07657769B
; Patent No. 5256766
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IRELL & MANELLA
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/657,769B
; FILING DATE: 19910219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0502:00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-657-769B-23

Query Match 48.8%; Score 21; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0;

Qy 4 MDPTP 8
: || |
Db 1 LDRP 5

RESULT 8

US-07-657-769B-62

; Sequence 62, Application US/07657769B

; Patent No. 5256766

; GENERAL INFORMATION:

; APPLICANT: COUGHLIN, SHAUN R.

; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED

; PHARMACEUTICALS

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: IRELL & MANELLA

; STREET: 545 MIDDLEFIELD ROAD, SUITE 200

; CITY: MENLO PARK

; STATE: CA

; COUNTRY: USA

; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/657,769B

; FILING DATE: 19910219

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MURASHIGE, KATE H.

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 2000-0502.00

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-327-7250

; TELEFAX: 415-327-2951

; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 62:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

US-07-657-769B-62

Query Match 48.8%; Score 21; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0;

Qy 4 MDPTP 8
: || |
Db 1 LDRP 5

RESULT 9

US-08-335-198-20

; Sequence 20, Application US/08335198

; Patent No. 5637454

; GENERAL INFORMATION:

; APPLICANT: Harley, John B.

; TITLE OF INVENTION: Assays and Treatments for Autoimmune

; DISEASES

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kilpatrick & Cody

; STREET: 1100 Peachtree Street, Ste. 2800

; CITY: Atlanta

; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30309-4539
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,198
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 07/648205
; APPLICATION NUMBER: US 07/648205
; FILING DATE: 01-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF 114CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)815-6508
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-335-198-20

Query Match 48.8%; Score 21; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0;

Qy 1 LKAMD 5
: || |
Db 1 LKALD 5

RESULT 10

US-07-789-184-68

; Sequence 68, Application US/07789184

; Patent No. 5688768

; GENERAL INFORMATION:

; APPLICANT: COUGHLIN, SHAUN R.

; APPLICANT: SCARBOROUGH, ROBERT M.

; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND

; RELATED PHARMACEUTICALS

; NUMBER OF SEQUENCES: 223

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/789,184

; FILING DATE: 19911107

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 22000-20502.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 34-0154
 INFORMATION FOR SEQ ID NO: 68:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-07-789-184-68

Query Match 48.8%; Score 21; DB 1; Length 5;
 Best Local Similarity 60.0%; Pred. No. 4.1e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDPTP 8
 :|||
 Db 1 LDRP 5

RESULT 11

US-08-475-263-68
 ; Sequence 68, Application US/08475263
 ; Patent No. 5759994
 ; GENERAL INFORMATION:
 ; APPLICANT: COUGHLIN, SHAUN R.
 ; APPLICANT: SCARBOROUGH, ROBERT M.
 ; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
 ; TITLE OF INVENTION: RELATED PHARMACEUTICALS
 ; NUMBER OF SEQUENCES: 223
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20006-1812
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/475,263
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 22000-20502.03
 ; TELEPHONE: (202) 887-1500
 ; TELEFAX: (202) 887-0763
 ; TELEX: 90-4030
 ; INFORMATION FOR SEQ ID NO: 68:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-475-263-68

Query Match 48.8%; Score 21; DB 1; Length 5;
 Best Local Similarity 60.0%; Pred. No. 4.1e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDPTP 8
 :|||
 Db 1 LDRP 5

RESULT 12
 US-08-485-886-68
 ; Sequence 68, Application US/08485886
 ; Patent No. 5798248
 ; GENERAL INFORMATION:
 ; APPLICANT: COUGHLIN, SHAUN R.
 ; APPLICANT: SCARBOROUGH, ROBERT M.
 ; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
 ; TITLE OF INVENTION: RELATED PHARMACEUTICALS
 ; NUMBER OF SEQUENCES: 223
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/485,886
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/789,184
 ; FILING DATE: 07-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 22000-20502.20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 34-0154
 ; INFORMATION FOR SEQ ID NO: 68:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-485-886-68

Query Match 48.8%; Score 21; DB 1; Length 5;
 Best Local Similarity 60.0%; Pred. No. 4.1e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDPTP 8
 :|||
 Db 1 LDRP 5

RESULT 13

US-08-477-362-68
 ; Sequence 68, Application US/08477362
 ; Patent No. 5849507
 ; GENERAL INFORMATION:
 ; APPLICANT: COUGHLIN, SHAUN R.
 ; APPLICANT: SCARBOROUGH, ROBERT M.
 ; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
 ; TITLE OF INVENTION: RELATED PHARMACEUTICALS
 ; NUMBER OF SEQUENCES: 223
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:

;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/477,362
;/ FILING DATE: 07-JUN-1995
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/789,184
;/ FILING DATE: 07-NOV-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: MURASHIGE, KATE H.
;/ REGISTRATION NUMBER: 29,959
;/ REFERENCE/DOCKET NUMBER: 22000-20502.20
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 813-5600
;/ TELEFAX: (415) 494-0792
;/ TELEX: 34-0154
;/ INFORMATION FOR SEQ ID NO: 68:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 5 amino acids
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-477-362-68

Query Match 48.8%; Score 21; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 MDPTP 8
Db 1 LDPRP 5

RESULT 14
US-08-477-134-68
;/ Sequence 68, Application US/08477134
;/ Patent No. 5856448
;/ GENERAL INFORMATION:
;/ APPLICANT: COUGHLIN, SHAUN R.
;/ APPLICANT: SCARBOROUGH, ROBERT M.
;/ TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
;/ TITLE OF INVENTION: RELATED PHARMACEUTICALS
;/ NUMBER OF SEQUENCES: 223
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: MORRISON & FOERSTER
;/ STREET: 755 Page Mill Road
;/ CITY: Palo Alto
;/ STATE: California
;/ COUNTRY: USA
;/ ZIP: 94304-1018
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/477,134
;/ FILING DATE: 07-JUN-1995
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/789,184
;/ FILING DATE: 07-NOV-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: MURASHIGE, KATE H.
;/ REGISTRATION NUMBER: 29,959
;/ REFERENCE/DOCKET NUMBER: 22000-20502.20
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 813-5600
;/ TELEFAX: (415) 494-0792
;/ TELEX: 34-0154

;/ INFORMATION FOR SEQ ID NO: 68:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 5 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-477-134-68

Query Match 48.8%; Score 21; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 MDPTP 8
Db 1 LDPRP 5

RESULT 15
US-08-473-489A-68
;/ Sequence 68, Application US/08473489A
;/ Patent No. 6024936
;/ GENERAL INFORMATION:
;/ APPLICANT: COUGHLIN, SHAUN R.
;/ APPLICANT: SCARBOROUGH, ROBERT M.
;/ TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
;/ TITLE OF INVENTION: RELATED PHARMACEUTICALS
;/ NUMBER OF SEQUENCES: 223
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: MORRISON & FOERSTER
;/ STREET: 755 Page Mill Road
;/ CITY: Palo Alto
;/ STATE: California
;/ COUNTRY: USA
;/ ZIP: 94304-1018
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/473,489A
;/ FILING DATE:
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US/07/789,184
;/ FILING DATE: 1991-11-07
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: MURASHIGE, KATE H.
;/ REGISTRATION NUMBER: 29,959
;/ REFERENCE/DOCKET NUMBER: 22000-20502.20
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 813-5600
;/ TELEFAX: (415) 494-0792
;/ TELEX: 34-0154
;/ INFORMATION FOR SEQ ID NO: 68:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 5 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-473-489A-68

Query Match 48.8%; Score 21; DB 3; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 MDPTP 8
Db 1 LDPRP 5

Search completed: May 26, 2005, 20:45:44
Job time : 42 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:26:23 ; Search time 15.8 Seconds
(without alignments)
60.897 Million cell updates/sec

Title: US-10-047-945-1

Perfect score: 54

Sequence: 1 LKAMDPTPPL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	77.8	398	2 A81717	conserved hypotet-
2	38	70.4	792	2 T29187	hypothetical prote
3	38	70.4	1325	2 S62497	probable nucleopor
4	37	68.5	142	2 A51681	similar o transcri
5	37	68.5	212	2 C87585	hypothetical prote
6	37	68.5	237	2 A42013	alpha-1-B-glycopro
7	37	68.5	286	2 S72384	hypothetical prote
8	37	68.5	429	2 S09852	hypothetical prote
9	37	68.5	450	2 B47265	tailless (tll) pro
10	37	68.5	452	2 A35602	tailless (tll) pro
11	37	68.5	1819	2 T32008	hypothetical prote
12	36	66.7	117	2 A53139	hypothetical prote
13	36	66.7	222	2 C71955	hypothetical prote
14	36	66.7	365	2 P87552	dnrA protein (lipo
15	36	66.7	392	2 T29519	hypothetical prote
16	36	66.7	431	2 T29716	hypothetical prote
17	36	66.7	460	2 H70986	hypothetical prote
18	36	66.7	490	2 T49096	hypothetical prote
19	36	66.7	898	2 T21179	hypothetical prote
20	36	66.7	944	2 A89624	protein P21A10-2 [
21	36	66.7	968	2 T46568	ATP-dependent RNA
22	36	66.7	2717	2 A34203	DNA-binding protei
23	35	64.8	159	2 S61040	probable membrane
24	35	64.8	206	2 S50913	TAF25 protein - ye
25	35	64.8	262	2 E64679	tryptophan synthas
26	35	64.8	291	2 AH2017	lipotic acid synth
27	35	64.8	313	2 A95859	conserved hypotet
28	35	64.8	323	1 TWMVF6	protein kinase (EC
29	35	64.8	380	1 TVFVNM	protein kinase (EC

30 35 64.8 382 1 TVBEG1 protein kinase (EC
31 35 64.8 382 1 TVBEXA protein kinase (EC
32 35 64.8 384 2 T42612 probable protein k
33 35 64.8 543 2 A53790 cytochrome P450-Ef
34 35 64.8 587 2 140849 succinate dehydrog
35 35 64.8 602 1 TVRTRR protein kinase (EC
36 35 64.8 627 2 T18772 hypotetrical prote
37 35 64.8 647 1 S00644 protein kinase raf
38 35 64.8 648 1 TVRTRF protein kinase raf
39 35 64.8 648 1 TVRTRF protein kinase raf
40 35 64.8 648 2 A25047 beta-glucuronidase
41 35 64.8 657 2 A53545 protein p84 - huma
42 35 64.8 678 2 T50256 probable vacuolar
43 35 64.8 765 2 T35719 chitinase - Strept
44 35 64.8 825 1 EDBEXD immediate-early pr
45 35 64.8 1397 2 T46354 hypotetrical prote

ALIGNMENTS

RESULT 1

A81717

conserved hypothetical protein TC0306 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: A81717

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: A81717

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-398 <TET>

A:Cross-references: UNIPROT:Q9PL02; GB:AE002298; GB:AE002160; NID:g7190343; PIDN:AAF3917

A:Experimental source: strain Nigg (MoPn)

C:Genetics:

A:Gene: TC0306

C:Superfamily: Chlamydia trachomatis hypotetrical protein CT036

Query Match 77.8%; Score 42; DB 2; Length 398;
Best Local Similarity 77.8%; Pred. No. 8.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTPPL 10
| : |||||
Db 309 KELDPTPPL 317

RESULT 2

T29187

hypothetical protein C55C3.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T29187

R:Woesne, J.; Steillyes, L.

submitted to the EMBL Data Library, April 1996

A:Description: The sequence of C. elegans cosmid C55C3.

A:Reference number: Z20585

A:Accession: T29187

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-792 <WOE>

A:Cross-references: EMBL:U53335; PIDN:AAA96170.1; GSPDB:GN00022; CESP:C55C3.3

A:Experimental source: strain Bristol N2; clone C55C3

C:Genetics:

A:Gene: CESP:C55C3.3

A:Map position: 4

A:Introns: 17/1; 46/3; 139/2; 173/1; 204/3; 250/3; 266/3; 286/2; 327/1; 362/3; 393/3; 43

Query Match

70.4%; Score 38; DB 2; Length 792;

Best Local Similarity 87.5%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTTP 8
|| |||||
DB 133 LKMPDTP 140

RESULT 3
S62497
probable nucleoporin - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C>Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S62497; T38281
R:Niblett, D.; Harris, D.
submitted to the EMBL Data Library, October 1995
A:Reference number: S62492
A:Accession: S62497
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1325 <NIB>
A:Cross-references: UNIPROT:Q09847; EMBL:Z64354; NID:g1039338; PIDN:CAA91241.1; PID:g103
R:Niblett, D.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z21783
A:Accession: T38281
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1325 <NID>
A:Cross-references: EMBL:Z64354; PIDN:CAA91241.1; GSPDB:GN00066; SPDB:SPAC23D3.06C
A:Experimental source: strain 972h-; cosmid c23D3
C:Genetics:
A:Gene: SPAC23D3.06C
A:Map position: 1R
A:Introns: 33/3

Query Match 70.4%; Score 38; DB 2; Length 1325;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMDPTTP 9
|| |||||
DB 299 KAGDPTTP 306

RESULT 4
AE1681
similar o transcription regulators lin1991 [imported] - *Listeria innocua* (strain Clip112
C:Species: *Listeria innocua*
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE1681
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Sincos, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative Genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1681
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <GLA>
A:Cross-references: UNIPROT:Q92AD1; GB:AL592022; PIDN:CAC97221.1; PID:g16414492; GSPDB:G
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin1991
C:Superfamily: conserved hypothetical protein MJ0568

Query Match 68.5%; Score 37; DB 2; Length 142;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTTP 9
|| |||||
DB 130 LKEMDTPK 138

RESULT 5
C87585
hypothetical protein CC2714 [imported] - *Caulobacter crescentus*
C:Species: *Caulobacter crescentus*
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: C87585
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Neilson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: AB7249; MUID:21173698; PMID:11259647
A:Accession: C87585
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-212 <STO>
A:Cross-references: UNIPROT:Q9A4W1; GB:AE005673; NID:g13424303; PIDN:AAK24679.1; GSPDB:C
C:Genetics:
A:Gene: CC2714

Query Match 68.5%; Score 37; DB 2; Length 212;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 KAMDPTTP 9
::: |||||
DB 52 RSLDPTTP 59

RESULT 6
A42013
alpha-1-B-glycoprotein - North American opossum (fragments)
C:Species: *Didelphis virginiana*, *Didelphis marsupialis virginiana* (North American opossum)
C>Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C:Accession: A42013
R:Catanesse, J.J.; Kress, L.F.
Biochemistry 31, 410-418, 1992
A:Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hu
A:Reference number: A42013; MUID:92118834; PMID:1731898
A:Accession: A42013
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-237 <CAT>
A:Cross-references: UNIPROT:Q28359; GB:J05356
C:Keywords: glycoprotein

Query Match 68.5%; Score 37; DB 2; Length 237;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPL 10
|| |||||
DB 1 LKAMDTTPRL 10

RESULT 7
S72384
hypothetical protein 8 precursor - *Enterococcus faecalis* plasmid pAD1
C:Species: *Enterococcus faecalis*
C>Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: S72384
R:Hirt, H.; Wirth, R.; Muscholl, A.
Mol. Gen. Genet. 252, 640-647, 1996
A:Title: Comparative analysis of 18 sex pheromone plasmids from *Enterococcus faecalis*:
A:Reference number: S72375; MUID:97074879; PMID:8917306
A:Accession: S72384
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A;Residues: 1-286 <HIR>
A;Cross-references: UNIPROT:Q47791; EMBL:X96977; NID:g1279406; PIDN:CAA65667.1; PID:g1279406
A;Experimental source: strain OGIX
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C;Genetics:
A;Genome: plasmid PAD1
C;Superfamily: probable pheromone-responsive protein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-286/Product: hypothetical protein 8 #status predicted <MAT>

Query Match 68.5%; Score 37; DB 2; Length 286;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KAMDPTPPL 10
|:|:|:|:|
Db 50 KPTDTPPI 58

RESULT 8
S09852
hypothetical protein UL88 - human cytomegalovirus (strain AD169)
C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S09852
C;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.; M.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
A;Reference number: S09749; MUID:90269039; PMID:2161319
A;Accession: S09852
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-429 <CHE>
A;Cross-references: UNIPROT:P16731; EMBL:X17403; NID:g59591; PIDN:CAA3362.1; PID:g17808
A;Note: this sequence was submitted to the EMBL Data Library, December 1989

Query Match 68.5%; Score 37; DB 2; Length 429;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTPP 9
|:|:|:|:|
Db 348 LEALDPTPP 356

RESULT 9
B47265
tailless (tll) protein - fruit fly (Drosophila virilis)
C;Species: Drosophila virilis
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
C;Accession: B47265
R;Liaw, G.J.; Steingrimsen, E.; Pignoni, F.; Courey, A.J.; Lengyel, J.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 858-862, 1993
A;Title: Characterization of downstream elements in a Raf-1 pathway.
A;Reference number: A47265; MUID:93157371; PMID:8430097
A;Accession: B47265
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 <LIA>
A;Cross-references: GB:L04955
C;Genetics:
A;Gene: FlyBase:Dvir/tll
A;Cross-references: FlyBase:FBgn0013145
C;Superfamily: erba transforming protein homology
C;Keywords: zinc finger
F;32-339/Domain: erba transforming protein homology <ERBA>

Query Match 68.5%; Score 37; DB 2; Length 450;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTPPL 10
|:|:|:|:|
Db 216 RALPPTPPL 224

RESULT 10
A35602
tailless (tll) protein - fruit fly (Drosophila melanogaster)
N;Alternate names: steroid hormone receptor homolog tll; transcription factor tll
C;Species: Drosophila melanogaster
C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 09-Jul-2004
C;Accession: A35602; A47265
R;Pignoni, F.; Baldarelli, R.M.; Steingrimsen, E.; Diaz, R.J.; Patapoutian, A.; Merriam
Cell 62, 151-163, 1990
A;Title: The Drosophila gene tailless is expressed at the embryonic termini and is a mem
A;Reference number: A35602; MUID:90304905; PMID:2364433
A;Accession: A35602
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-452 <PIG>
A;Cross-references: UNIPROT:P18102; GB:X52147
R;Liaw, G.J.; Steingrimsen, E.; Pignoni, F.; Courey, A.J.; Lengyel, J.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 858-862, 1993
A;Title: Characterization of downstream elements in a Raf-1 pathway.
A;Reference number: A47265; MUID:93157371; PMID:8430097
A;Accession: A47265
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-452 <LIA>
A;Cross-references: GB:AF019362; GB:L04954; NID:g2429340; PIDN:AAB71371.1; PID:g2440022
A;Note: sequence extracted from NCBI backbone (NCBIN:124057, NCBIP:124058)
C;Genetics:
A;Gene: tll
A;Cross-references: FlyBase:FBgn0003720
A;Note: tailless
C;Superfamily: unassigned erba-related proteins; erba transforming protein homology
C;Keywords: DNA binding; steroid hormone receptor; transcription regulation; zinc finger
F;32-341/Domain: erba transforming protein homology <ERBA>

Query Match 68.5%; Score 37; DB 2; Length 450;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTPPL 10
|:|:|:|:|
Db 218 RALPPTPPL 226

RESULT 11
T32008
hypothetical protein K10G6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32008
R;Davidson, S.; Wohldmann, P.; Mullen, G.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid K10G6.
A;Reference number: Z2111
A;Accession: T32008
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1819 <DAV>
A;Cross-references: UNIPROT:O16625; EMBL:AF016669; PIDN:AAB66098.1; GSPDB:GN00020; CESP:
A;Experimental source: strain Bristol N2; clone K10G6
C;Genetics:
A;Gene: CESP:K10G6.3
A;Map position: 2
A;Introns: 41/2; 191/2; 556/2; 701/2; 1645/2; 1700/2; 1768/1; 1797/3

Query Match 68.5%; Score 37; DB 2; Length 1819;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPP 9
| :|||||
Db 500 LMTLDTTP 508

RESULT 12

AF3319
hypothetical protein BMEI0540 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AF3319
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujeer, C.; Los, T.; Ivanova, .; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessé Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AF3319
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <KUR>
A:Cross-references: UNIPROT:OBYIA5; GB:AE008917; PIDN:AAL51721.1; PID:gl7982457; GSPDB:C
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0540.
A:Map position: 1

Query Match 66.7%; Score 36; DB 2; Length 117;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMDPTPPL 10
| :|||||
Db 83 KACDPLPPM 91

RESULT 13

C71955
hypothetical protein jhp0241 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: C71955
R:Ahm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; PMID:99120557; PMID:9923682
A:Accession: C71955
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <ARN>
A:Cross-references: UNIPROT:Q9ZMH9; GB:AE001462; GB:AE001439; NID:g4154760; PIDN:AAD0583
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0241

Query Match 66.7%; Score 36; DB 2; Length 222;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMDPTPP 9
| :|||||
Db 193 KTTDPTTP 200

RESULT 14

F87552
dprA protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: F87552
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: F87552
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-365 <STO>
A:Cross-references: UNIPROT:Q9A5K0; GB:AE005673; NID:gl13423992; PIDN:AAK24418.1; GSPDB:B
C:Genetics:
A:Gene: CC2447

Query Match 66.7%; Score 36; DB 2; Length 365;
Best Local Similarity 60.0%; Pred. No. 88;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
| :|||||
Db 92 LAALDPPPPV 101

RESULT 15

T29519
hypothetical protein T25F10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29519
R:Pauley, A.; Gattung, S.
A:Title: submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid T25F10.
A:Reference number: Z20634
A:Accession: T29519
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-392 <PAU>
A:Cross-references: UNIPROT:Q23048; EMBL:U64856; PIDN:AAB04987.1; GSPDB:GN00023; CESP:T2
A:Experimental source: strain Bristol N2; clone T25F10
C:Genetics:
A:Gene: CESP.T25F10.4
A:Map position: 5
A:Introns: 38/3; 84/2; 156/3; 182/3; 228/3; 256/1; 312/2; 337/3; 361/2

Query Match 66.7%; Score 36; DB 2; Length 392;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPTPPL 10
| :|||||
Db 291 DPTPPL 296

Search completed: May 26, 2005, 18:44:43
Job time : 18.8 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:18:07 ; Search time 76.4 Seconds
(without alignments)
67.026 Million cell updates/sec

Title: US-10-047-945-1
Perfect score: 54
Sequence: 1 LKAMDPTPPL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	17	2 Q9TR78	Q9tr78 didelphis m
2	54	100.0	291	1 DM43_DIDMR	P82957 didelphis m
3	45	83.3	140	2 Q8HZ75	Q8hz75 didelphis m
4	45	83.3	291	2 Q8HZ74	Q8hz74 didelphis m
5	42	77.8	398	1 X306_CHLMU	Q3pl02 chlamydia m
6	41	75.9	99	2 Q6CS47	Q6cs47 kluyveromyc
7	41	75.9	165	2 Q9W3H5	Q9w3h5 drosophila
8	39	72.2	98	2 Q853J7	Q853j7 mycobacteri
9	39	72.2	156	2 Q8MLX6	Q8mlx6 echinococcu
10	39	72.2	227	2 Q732B2	Q732b2 mycobacteri
11	39	72.2	243	2 Q96ID3	Q96id3 homo sapien
12	39	72.2	268	2 Q6GIP6	Q6gip6 bartonella
13	39	72.2	320	2 Q8V3M1	Q8v3m1 swinepox vi
14	39	72.2	693	2 Q9K437	Q9k437 streptomyce
15	39	72.2	754	1 KB15_HUMAN	Q9upn7 homo sapien
16	39	72.2	849	2 Q6NVJ6	Q6nvj6 homo sapien
17	38	70.4	86	2 Q6FVQ3	Q6fvq3 candida gla
18	38	70.4	274	2 Q95Q06	Q95q06 caenorhabdi
19	38	70.4	302	2 Q8CBA3	Q8cba3 mus musculu
20	38	70.4	369	2 Q96532	Q96532 arabidopsis
21	38	70.4	369	2 Q42606	Q42606 arabidopsis
22	38	70.4	560	2 Q6C7D9	Q6c7d9 yarrowia li
23	38	70.4	881	2 Q3NE42	Q3ne42 leishmania
24	38	70.4	1325	1 YAE6_SCHPO	Q9847 schizosacch
25	38	70.4	1345	2 Q8CIP5	Q8cip5 mus musculu
26	37	68.5	70	2 Q7PIK7	Q7pik7 anopheles g
27	37	68.5	107	2 Q36604	Q36604 hepatitis e
28	37	68.5	142	1 MNTR_LISIN	Q32adl listeria in
29	37	68.5	156	2 Q8WPI6	Q8wpi6 echinococcu
30	37	68.5	212	2 Q9A4W1	Q9a4w1 caulobacter
31	37	68.5	242	2 Q8BXK6	Q8bxk6 mus musculu

32	37	68.5	255	2	Q67PT6	Q67pt6 symbiobacte
33	37	68.5	270	2	Q8KUD2	Q8kud2 enterococcu
34	37	68.5	271	2	Q838G9	Q838g9 enterococcu
35	37	68.5	286	2	Q47791	Q47791 enterococcu
36	37	68.5	286	2	Q9F1F9	Q9f1f9 enterococcu
37	37	68.5	286	2	Q82YS6	Q82ys6 enterococcu
38	37	68.5	314	2	Q8HYX5	Q8hyx5 didelphis m
39	37	68.5	316	2	Q6NAY5	Q6nay5 rhodopsu
40	37	68.5	393	2	Q7QJ80	Q70j80 streptomyce
41	37	68.5	429	1	UL88_HCMVA	P16731 human cytom
42	37	68.5	429	2	Q7M6K3	Q7m6k3 human cytom
43	37	68.5	450	1	TLL_DROVI	O16845 drosophila
44	37	68.5	452	1	TLL_DROME	P18102 drosophila
45	37	68.5	699	2	Q7RV16	Q7rv16 neurospora

ALIGNMENTS

RESULT 1

Q9TR78 PRELIMINARY; PRT; 17 AA.
AC Q9TR78
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-BOTHRPIC complex 48,000 SUBUNIT (Fragment).
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE.
RX MEDLINE=95149299; PubMed=7846694; DOI=10.1016/0041-0101(94)90353-0;
RA Perales J., Mousasche H., Marangoni S., Oliveira B., Domont G.B.;
RT "Isolation and partial characterization of an anti-bothropic complex
RT from the serum of South American Didelphidae.";
RL Toxicol 32:1237-1249(1994).
SQ SEQUENCE 17 AA; 1947 MW; CB55FB40E73B2A2A CRC64;

Query Match 100.0%; Score 54; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10

Db 1 LKAMDPTPPL 10

RESULT 2

DM43_DIDMR STANDARD; PRT; 291 AA.
AC P82957; 291 AA, Created
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom metalloproteinase inhibitor DM43.
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Serum;
RA MEDLINE=21953368; PubMed=11815628; DOI=10.1074/jbc.M200589200;
RA Neves-Ferreira A.G.C., Perales J., Fox J.W., Shannon J.D.,
RA Makino D.L., Garratt R.C., Domont G.B.;
RT "Structural and functional analyses of DM43, a snake venom
RT metalloproteinase inhibitor from Didelphis marsupialis serum.";
RL J. Biol. Chem. 277:13129-13137(2002).
CC -|- FUNCTION: Metalloproteinase inhibitor.
CC -|- SUBUNIT: Homodimer.
CC -|- TISSUE SPECIFICITY: Blood and milk.

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CC -!- PTM: N-glycosylated.
CC -!- MASS SPECTROMETRY: MW=42691; METHOD=MALDI; RANGE=1-291;
CC NOTE=Ref 1.
CC
CC -!- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR011015; LEM_like.
DR Pfam; PF00047; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Metalloprotease inhibitor; Repeat.
FT DOMAIN 22 79 IG-like V-type 1.
FT DOMAIN 114 171 IG-like V-type 2.
FT DOMAIN 191 288 IG-like V-type 3.
FT DISULFID 28 74 Potential.
FT DISULFID 121 163
FT DISULFID 213 285
FT CARBOHYD 23 23 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 156 156 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 160 160 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 175 175 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 291 AA; 32390 MW; 17A496227869A65B CRC64;

Query Match 100.0%; Score 54; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. NO. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
DB 1 LKAMDPTPPL 10

RESULT 3
QBH275 PRELIMINARY; PRT; 140 AA.
AC Q8H275;
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha 1B glycoprotein DVOP51-D (Fragment).
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
ON NCBI_TaxID=9267;
RX SEQUENCE FROM N.A.
RA Martinez M.E., Pierce J.R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV131000; AAN06911.1; -.
DR HSP; O76036; IOLL.
DR InterPro; IPR007110; IG-like.
FT NON_TER 1
FT NON_TER 140
SQ SEQUENCE 140 AA; 15297 MW; E19D071A76AA5A7F CRC64;

Query Match 83.3%; Score 45; DB 2; Length 140;
Best Local Similarity 90.0%; Pred. NO. 6.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
DB 42 LKAMDPTPPL 51

RESULT 4
QBH274 PRELIMINARY; PRT; 291 AA.
AC Q8H274;
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha 1B glycoprotein DVOP114 (Fragment).
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Martinez M.E., Pierce J.R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV131001; AAN06912.1; -.
DR HSP; Q8NHL6; IGOX.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 291
SQ SEQUENCE 291 AA; 32509 MW; BEC282838A1C0BF4 CRC64;

Query Match 83.3%; Score 45; DB 2; Length 291;
Best Local Similarity 90.0%; Pred. NO. 14;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
DB 1 LKAMDPTPPL 10

RESULT 5
Y306 CHLMU STANDARD; PRT; 398 AA.
ID Y306 CHLMU
AC Q9PL02;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein TC0306.
OS OrderedLocustNames=TC0306;
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MoPn / Nig9;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Uterback T.R., Berry K.J.,
RA Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
RA Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.P.,
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the chlamydial CPN0129/CP036/TC0306 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE002298; AAF39171.1; -.
DR FIR; AB1717; AB1717.
DR TIGR; TC0306; -.
KW Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 31 Potential.
FT TRANSMEM 56 76 Potential.
SQ SEQUENCE 398 AA; 44639 MW; 8CD8E541C5C92A88 CRC64;

Query Match 77.8%; Score 42; DB 1; Length 398;
Best Local Similarity 77.8%; Pred. NO. 66;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      2 KAMDPTTLP 10
DB      309 KELDPTTLP 317

RESULT 6
QCS47   PRELIMINARY;      PRT;      99 AA.
ID      Q6CS47;
AC      Q6CS47;
DT      25-OCT-2004 (TrEMBLrel. 28, Created)
DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE      Similar to sg|S0007245 Saccharomyces cerevisiae YLL018ca COX19.
GN      ORFNames=KLA0D03971g;
OS      Kluyveromyces lactis NRRL Y-1140.
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX      NCBI_TaxID=284590;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NRRL Y-1140;
RG      Genolevures;
RA      Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA      Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talia E.,
RA      Goffard N., Franchou L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA      Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA      Boierane A., Boyer J., Battolico L., Confaniolieri F., de Daruvar A.,
RA      Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA      Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA      Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA      Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA      Pellenz S., Potier S., Richard G.P., Straub M.L., Suleau A.,
RA      Swennene D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA      Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA      Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA      Wincker P., Souciet J.L.;
RT      "Genome evolution in yeasts.";
RL      Nature 430:35-44(2004).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NRRL Y-1140;
RG      Genoscope;
RA      Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; CR382124; CAH00338.1; -.
DR      InterPro; IPR010625; CHCH.
DR      Pfam; PF06747; CHCH, 1.
SQ      SEQUENCE 99 AA; 11050 MW; 032BA5DD3C50CAC2 CRC64;

Query Match      75.9%; Score 41; DB 2; Length 99;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKAMDPTTTP 9
DB      9 LKALSPTTP 17

RESULT 7
ID      Q9W3H5;      PRELIMINARY;      PRT;      165 AA.
AC      Q9W3H5;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE      CG2147-PA (LP02728p).
GN      ORFNames=CG2147;
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]

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RP      SEQUENCE FROM N.A.
RX      MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA      Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA      Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA      George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA      Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA      Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA      Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA      Abill J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,
RA      Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA      Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA      Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA      Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA      Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA      de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA      Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA      Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA      Foster C., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA      Glodek A., Gong P., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA      Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA      Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA      Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA      Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA      Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA      Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA      Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA      Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA      Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA      Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA      Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA      Spier E., Stadling A.C., Stapleton M., Strong R., Sun E.,
RA      Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
RA      Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA      Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA      Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA      Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA      Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT      "The genome sequence of Drosophila melanogaster.";
RL      Science 287:2185-2195(2000).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22426065; PubMed=12537568;
RA      Celnikier S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA      Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA      George R.A., Hoskins R.A., Laverdy T., Muzny D.M., Nelson C.R.,
RA      Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA      Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA      Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT      "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT      melanogaster euchromatic genome sequence.";
RL      Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22426070; PubMed=12537573;
RA      Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA      Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA      Ashburner M., Celnikier S.E.;
RT      "The transposable elements of the Drosophila melanogaster euchromatin:
RT      a genomics perspective.";
RL      Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN      [4]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22426069; PubMed=12537572;
RA      Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA      Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA      Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA      Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,
RA      Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA      Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA      Lewis S.E.;
RT      "Annotation of the Drosophila melanogaster euchromatic genome: a
RT      systematic review.";

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RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RN Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreenek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Facib J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003443; AAF46352.1; --
DR EMBL; AY069722; AAL39867.1; --
DR IntAct; Q9W3H5; --
DR FlyBase; FBgn0030025; CG2147.
SQ SEQUENCE 165 AA; 17157 MW; CF3E6D2E102302C2 CRC64;

Query Match 75.9%; Score 41; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPTPPL 10
Db |||||
1 MDPTPPL 7

RESULT 8
Q853J7 PRELIMINARY; PRT; 98 AA.
AC Q85J7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp80.
OS Mycobacteriophage Bx1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=205877;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;
RA Pedulla M.L., Ford M.E., Houtz J.M., Karkhikyan T., Wadsworth C.,
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Panunzio N.R.,
RA Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA Hatfull G.F.;
RT "Origins of highly mosaic mycobacteriophage genomes.";
DR Cell 113:171-182(2003).
RL EMBL; AY129337; AAN16740.1; --
SQ SEQUENCE 98 AA; 10867 MW; D1D8FE87C4CDD15E CRC64;

Query Match 72.2%; Score 39; DB 2; Length 98;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KAMDTPPP 9
Db :|||
29 QALDTPPP 36

RESULT 9
Q8MLX6 PRELIMINARY; PRT; 156 AA.
AC Q8MLX6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

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DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE EM95 vaccine antigen.
OS Echinococcus multilocularis.
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Taeniidae; Echinococcus.
OX NCBI_TaxID=6211;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22060722; PubMed=12065546;
RX DOI=10.1128/IAI.70.7.3969-3972.2002;
RA Gauci C., Merli M., Muller V., Chow C., Yagi K., Mackenstedt U.,
RA Lightowler M.W.;
RT "Molecular cloning of a vaccine antigen against infection with the
RT larval stage of Echinococcus multilocularis.";
RL Infect. Immun. 70:3969-3972(2002).
DR EMBL; AY082920; AAL51152.1; --
DR EMBL; AY082921; AAL51153.1; --
DR InterPro; IPR003961; FN III.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS00853; FN3; 1.
SQ SEQUENCE 156 AA; 17145 MW; F96E940A0D5B731D CRC64;

Query Match 72.2%; Score 39; DB 2; Length 156;
Best Local Similarity 70.0%; Pred. No. 76;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDTPPL 10
Db |||||
66 LKALDPSDPL 75

RESULT 10
Q73ZB2 PRELIMINARY; PRT; 227 AA.
AC Q73ZB2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS OrderedLocustNames=MAP1691c;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X10;
RA Li L., Bannantine J., Zhang Q., Anonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017233; AAS04008.1; --
KW Complete proteome.
SQ SEQUENCE 227 AA; 24027 MW; 952EA4962C0EE199 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 227;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDTPPL 10
Db |||||
146 LAALDPRPPL 155

RESULT 11
Q96ID3 PRELIMINARY; PRT; 243 AA.
AC Q96ID3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE KIAA1115 protein (Fragment).
GN Name=KIAA1115;
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_TaxID=9606;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.;
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC007629; AA07629.1; -;
 FT NON TER 1
 SQ SEQUENCE 243 AA; 24559 MW; 9094604DE493228 CRC64;
 Query Match 72.2%; Score 39; DB 2; Length 243;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 LKAMDPTPP 9
 Db 130 LRSQDPTPP 138
 ID Q6G1P6 PRELIMINARY; PRT; 268 AA.
 AC Q6G1P6
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE 1-acyl-sn-glycerol-3-phosphate acyltransferase.
 GN Name=plsc; OrderedLocNames=BH18290;
 OS Bartonella henselae (Rochalimaea henselae).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bartonellaceae; Bartonella.
 OX NCBI_TaxID=38323;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 49882 / Houston 1;
 RX PubMed=15210978; DOI=10.1073/pnas.0305659101;
 RA Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,
 RA Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvel M.,
 RA La Scola B., Holmberg M., Andersson S.G.E.;
 RT "The louse-borne human pathogen Bartonella quintana is a genomic
 RT derivative of the zoonotic agent Bartonella henselae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
 DR EMBL; BX897699; CAF28391.1; -;
 DR GO; GO:0008415; F:acyltransferase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002123; Acyltransferase.

DR Pfam; PF01553; Acyltransferase; 1.
 DR SMART; SMO0563; Plsc; 1.
 KW Acyltransferase; Complete proteome; Transferase.
 SQ SEQUENCE 268 AA; 30957 MW; 2F955B7EFBD8B95 CRC64;
 Query Match 72.2%; Score 39; DB 2; Length 268;
 Best Local Similarity 77.8%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 LKAMDPTPP 9
 Db 240 LAAQDPTPP 248
 ID Q8V3M1 PRELIMINARY; PRT; 320 AA.
 AC Q8V3M1
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE SPV074 DNA topoisomerase.
 GN Name=SPV074;
 OS Swinepox virus (SWPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Suipoxvirus.
 OX NCBI_TaxID=10276;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21624277; PubMed=11752168; DOI=10.1128/JVI.76.2.783-790.2002;
 RA Alfonso C.L., Tulman E.R., Lu Z., Zsak L., Osorio F.A., Balinsky C.,
 RA Kutish G.F., Rock D.L.;
 RT "The genome of swinepox virus.";
 RL J. Virol. 76:783-790(2002).
 DR EMBL; AF410153; AAL69813.1; -;
 DR HSP; P08585; 1VCC.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003917; F:DNA topoisomerase type I activity; IEA.
 DR GO; GO:0016853; F:isomerase activity; IEA.
 DR GO; GO:0006265; P:DNA topological change; IEA.
 DR GO; GO:0006268; P:DNA unwinding; IEA.
 DR Pfam; PF01028; Topoisom_I; 1.
 DR PRINTS; PR00416; EUTPISMRASEI.
 DR PROSITE; PS00176; TOPOISOMERASE_I_EUK; UNKNOWN_1.
 KW Isomerase.
 SQ SEQUENCE 320 AA; 38179 MW; 97F9B94442DD1DC5 CRC64;
 Query Match 72.2%; Score 39; DB 2; Length 320;
 Best Local Similarity 50.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 LKAMDPTPP 10
 Db 241 IKSLDPVPP 250
 ID Q9K437 PRELIMINARY; PRT; 693 AA.
 AC Q9K437
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative hydrolase.
 GN ORFNames=SCG22.08c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomyces; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;

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RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieseer H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieseer T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147 (2002).
DR EMBL; AL939107; CAB95281.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR006101; Glyco_hydro_2.
DR InterPro; IPR006102; Glyco_hydro_2lg.
DR InterPro; IPR006104; Glyco_hydro_2SB.
DR InterPro; IPR006103; Glyco_hydro_2TIM.
DR InterPro; IPR002088; PPTA.
DR Pfam; PF00703; Glyco_hydro_2; 1.
DR Pfam; PF02836; Glyco_hydro_2_C; 1.
DR Pfam; PF02837; Glyco_hydro_2_N; 1.
DR PRINTS; PR00132; GLHYDRLASE2.
DR PROSITE; PS00904; PPTA; UNKNOWN_1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 693 AA; 75941 MW; E54676BCCA33A921 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 693;
Best Local Similarity 70.0%; Pred. No. 4e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPL 10
Db 420 LKALDPTPLV 429
|||||
|:|:|:|:|

RESULT 15
KB15 HUMAN STANDARD; PRT; 754 AA.
AC Q9UPN7; Q9BU97;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein KIAA1115.
GN Name=KIAA1115;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
EX MEDLINE=99397452; PubMed=10470851;
RA Kikuno R., Nagase T., Iihikawa K.-I., Hirotsawa M., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:197-205(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins E.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SIMILARITY: Belongs to the SAPS family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB029038; BAA83067.2; ALT_INIT.
DR EMBL; BC002799; AAH02799.1; -.
DR IntAct; Q9UPN7; -.
DR InterPro; IPR007587; SAPS.
DR Pfam; PF04499; SAPS; 1.
DR DOMAIN 497 558 Glu-rich.
FT DOMAIN 570 751 Pro-rich.
FT DOMAIN 497 504 Poly-Glu.
FT DOMAIN 544 558 Poly-Glu.
FT CONFLICT 751 751 P -> S (in Ref. 1).
SQ SEQUENCE 754 AA; 82250 MW; 8B6964AE2226774E CRC64;

Query Match 72.2%; Score 39; DB 1; Length 754;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPP 9
Db 641 LRSQDPTPP 649
|:|:|:|:|

Search completed: May 26, 2005, 18:43:17
Job time : 79.4 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:17:22 ; Search time 86 Seconds
(without alignments)
44.972 Million cell updates/sec

Title: US-10-047-945-1

Perfect score: 54

Sequence: 1 LKAWDPTPPL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	2	AAW53843
2	54	100.0	10	7	ABB80222 N-terminu
3	54	100.0	11	7	ABB80222 Synthetic
4	54	100.0	12	7	ABB80225 Synthetic
5	54	100.0	15	2	AAW11575
6	54	100.0	15	2	AAW53841
7	54	100.0	15	7	ABB80223 Synthetic
8	50	92.6	9	7	ABB80227 Synthetic
9	43	79.6	8	7	ABB80228 Synthetic
10	42	77.8	94	4	AAO02179 Human pol
11	41	75.9	165	4	ABB58900 Drosophil
12	39	72.2	459	3	AAW53841 N-terminu
13	39	72.2	754	8	AAW53841 N-terminu
14	39	72.2	754	8	AAW53841 N-terminu
15	38	70.4	78	4	AAW53841 N-terminu
16	38	70.4	108	7	AAW53841 N-terminu
17	38	70.4	267	2	AAW53841 N-terminu
18	38	70.4	349	3	AAW53841 N-terminu
19	38	70.4	369	3	AAW53841 N-terminu
20	38	70.4	369	3	AAW53841 N-terminu
21	38	70.4	369	5	AAW53841 N-terminu
22	38	70.4	405	3	AAW53841 N-terminu
23	37	68.5	15	2	AAW53841 N-terminu
24	37	68.5	210	2	AAW53841 N-terminu
25	37	68.5	210	5	AAW53841 N-terminu

26	37	68.5	210	6	ABU88372
27	37	68.5	210	6	ABU13623
28	37	68.5	256	2	AAU00124
29	37	68.5	256	5	ABP43343
30	37	68.5	256	6	ABU88371
31	37	68.5	256	6	ABU13622
32	37	68.5	270	6	ABU23194
33	37	68.5	285	6	ABU28946
34	37	68.5	291	7	ADH88791
35	37	68.5	306	7	ADH88698
36	37	68.5	452	4	ABB58056
37	37	68.5	481	8	ADN25164
38	36	66.7	86	4	ABG17160
39	36	66.7	86	7	ADF60462
40	36	66.7	100	4	AAO09783
41	36	66.7	107	4	AAO06147
42	36	66.7	172	8	ABM82179
43	36	66.7	220	4	ABG26257
44	36	66.7	222	2	AAW55552
45	36	66.7	323	7	ABO67138

ALIGNMENTS

RESULT 1
AAW53843
ID AAW53843 standard; peptide; 10 AA.
XX
AC AAW53843;
XX
DT 08-JUL-1998 (first entry)
XX
DE N-terminus of opossum LTNF.
XX
KW LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;
KW anti-haemorrhagic protein; Elapidae; Viperae; sea snake; snake bite;
KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
KW histamine reaction treatment.
XX
OS Didelphis virginiana.
XX
FN US5744449-A.
XX
PD 28-APR-1998.
XX
PP 03-JUN-1996; 96US-00657163.
XX
PR 10-MAY-1993; 93US-00058387.
PR 22-SEP-1994; 94US-00310340.
PA (LIPP/) LIPPS B V.
PA (LIPP/) LIPPS F W.
XX
PI Lipps FW, Lipps BV;
XX WPI; 1998-271108/24.
XX
DR Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
XX venom(s) from all major families of poisonous snakes.
XX
CC Claim 7; Col 11; lipp; English.
XX
CC This sequence represents the peptide of the invention. It is a Lethal
XX Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic
XX protein derived from an opossum. The peptide can be used in a method for
XX treating a victim of envenomation from a poisonous snake, preferably a
XX poisonous snake from the family of Elapidae, Viperae or sea snake. It
XX is useful for the treatment of snake bites, sepsis, allergies caused by
XX the environment and treatment of bee or scorpion stings or toxicities
XX caused by plant or bacterial toxins. The peptide can also be used in
XX histamine reaction treatment. The peptide can be used in envenomation
XX treatment for a variety of snakes without prior identification of the

CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins

XX Sequence 10 AA;
 SQ Query Match 100.0%; Score 54; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTPPL 10
 |||||
 Db 1 LKAMDPTPPL 10

RESULT 2
 ABB80222
 ID ABB80222 standard; peptide; 10 AA.

XX AC ABB80222;
 XX 06-NOV-2003 (first entry)

XX DE Synthetic LTNF, LT-10.

XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.

XX OS Synthetic.

XX PN WO2003060471-A2.

XX PD 24-JUL-2003.

XX PF 14-JAN-2003; 2003WO-US001044.

XX PR 14-JAN-2002; 2002US-00047945.

XX PA (LIPP/) LIPPS B V.
 XX PA (LIPP/) LIPPS F W.

XX PI Lipps BV, Lipps FW;

XX DR WPI; 2003-636703/60.

XX PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

XX PS Claim 7; Page 3; 24pp; English.

XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IgE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX Sequence 10 AA;
 SQ Query Match 100.0%; Score 54; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10
 |||||
 Db 1 LKAMDPTPPL 10

RESULT 3
 ABB80226
 ID ABB80226 standard; peptide; 11 AA.

XX AC ABB80226;

XX DT 06-NOV-2003 (first entry)

XX DE Synthetic LTNF, LT-11.

XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.

XX OS Synthetic.

XX PN WO2003060471-A2.

XX PD 24-JUL-2003.

XX PF 14-JAN-2003; 2003WO-US001044.

XX PR 14-JAN-2002; 2002US-00047945.

XX PA (LIPP/) LIPPS B V.
 XX PA (LIPP/) LIPPS F W.

XX PI Lipps BV, Lipps FW;

XX DR WPI; 2003-636703/60.

XX PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

XX PS Claim 7; Page 4; 24pp; English.

XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IgE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX Sequence 11 AA;

```

- Query Match      100.0%; Score 54; DB 7; Length 11;
  Best Local Similarity 100.0%; Pred. No. 0.036;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10
Db 1 LKAMDPTPPL 10
    |||||
    |||||

RESULT 4
ABB80225
ID ABB80225 standard; peptide; 12 AA.
XX
AC ABB80225;
XX
DT 06-NOV-2003 (first entry)
XX
DE Synthetic LTNF, LT-12.
XX
KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW saliva; ELISA.
XX
OS Synthetic.
XX
XX WO2003060471-A2.
XX
XX 24-JUL-2003.
XX
XX 14-JAN-2003; 2003WO-US001044.
XX
XX 14-JAN-2002; 2002US-00047945.
XX
XX (LIPP/) LIPPS B V.
XX (LIPP/) LIPPS F W.
XX
XX Lipps BV, Lipps FW;
XX
XX WPI; 2003-636703/60.
XX
XX Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
XX insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
XX asthma or diabetes, by employing an ELISA on a saliva sample from a
XX patient.
XX
XX Claim 7; Page 4; 24pp; English.
XX
XX The sequences given in ABB80222-28 represent lethal toxin neutralising
XX factor (LTNF) peptides which may be used for reducing elevated levels of
XX serum proteins selected from immunoglobulin E (IgE), nerve growth factor
XX (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
XX particular, the methods of the invention are useful for diagnosing and
XX treating conditions with elevated serum IgE levels, e.g. asthma,
XX diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
XX arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
XX Addison's disease or Hodgkin's disease) or depression. The efficacy of
XX the protein may be monitored by assaying a human endogenous protein by
XX performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
XX sample using an anti-serum that is specific for the protein. Saliva
XX collection is relatively non-invasive when compared to blood collection
XX for serum. Saliva can be centrifuged immediately, whereas blood requires
XX clotting time before centrifugation to separate serum. Saliva proteins
XX can be assayed by a simple ELISA test, whereas an assay of proteins from
XX serum requires a more complicated sandwich type ELISA
XX
XX Sequence 12 AA;

Query Match      100.0%; Score 54; DB 7; Length 12;
  Best Local Similarity 100.0%; Pred. No. 0.039;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10
Db 1 LKAMDPTPPL 10
    |||||
    |||||

RESULT 5
AAW11575
ID AAW11575 standard; peptide; 15 AA.
XX
AC AAW11575;
XX
DT 25-MAR-2003 (revised)
DT 20-MAR-1997 (first entry)
XX
DE N-terminal peptide from lethal toxin neutralising factor.
XX
KW Lethal toxin neutralising factor; LTNF; opossum; bee toxin;
KW scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.
XX
OS Didelphis virginiana.
XX
XX US5576297-A.
XX
XX 19-NOV-1996.
XX
XX 22-SEP-1994; 94US-00310340.
XX
XX 10-MAY-1993; 93US-00058387.
XX
XX (LIPP/) LIPPS B V.
XX (LIPP/) LIPPS F W.
XX
XX Lipps FW, Lipps BV;
XX
XX WPI; 1997-011287/01.
XX
XX Treatment of victims of bee or scorpion stings or plant or bacterial
XX toxins - by admin. of lethal toxin-neutralising factor or its N-terminal
XX peptide.
XX
XX Claim 7; Col 9; 9pp; English.
XX
XX The present sequence is from the N-terminus of a 68 kD protein purified
XX from the serum of the opossum Didelphis virginiana. The full-length
XX protein is a lethal toxin neutralising factor (LTNF). The use of purified
XX LTNF or of the chemically synthesised 15mer N-terminal peptide for
XX treating victims of bee stings, scorpion stings and bacterial or plant
XX toxins is claimed. The patent disclosure does not provide any evidence
XX for neutralising activity against these various toxins. There is evidence
XX of significant neutralising activity of the opossum LTNF and the 15mer
XX peptide against venom from snakes of the families Crotalidae, Elaphidae,
XX Hydroliidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 15 AA;

Query Match      100.0%; Score 54; DB 2; Length 15;
  Best Local Similarity 100.0%; Pred. No. 0.049;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10
Db 1 LKAMDPTPPL 10
    |||||
    |||||

RESULT 6
AAW53841
ID AAW53841 standard; peptide; 15 AA.
XX
AC AAW53841;
XX
XX 08-JUL-1998 (first entry)
XX

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DE N-terminus of opossum LTNF.
 XX
 KW LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;
 KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
 KW histamine reaction treatment.
 XX
 OS Didelphis virginiana.
 XX
 PN US5744449-A.
 XX
 PD 28-APR-1998.
 XX
 XX 03-JUN-1996; 96US-00657163.
 XX
 PR 10-MAY-1993; 93US-00058387.
 PR 22-SEP-1994; 94US-00310340.
 XX
 PA (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.
 XX
 PI Lipps FW, Lipps BV;
 XX
 XX WPI; 1998-271108/24.
 DR
 XX Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
 PT venom(s) from all major families of poisonous snakes.
 PT
 XX Claim 1; Col 11; lipp; English.
 PS
 XX This sequence represents the peptide of the invention. It is a Lethal
 CC Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic
 CC protein derived from an opossum. The peptide can be used in a method for
 CC treating a victim of envenomation from a poisonous snake, preferably a
 CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
 CC is useful for the treatment of snake bites, sepsis, allergies caused by
 CC the environment and treatment of bee or scorpion stings or toxicities
 CC caused by plant or bacterial toxins. The peptide can also be used in
 CC histamine reaction treatment. The peptide can be used in envenomation
 CC treatment for a variety of snakes without prior identification of the
 CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins
 CC
 XX Sequence 15 AA;
 SQ
 Query Match 100.0%; Score 54; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTPPL 10
 Db 1 LKAMDPTPPL 10
 |||||
 RESULT 7
 ABB80223
 ID ABB80223 standard; peptide; 15 AA.
 AC ABB80223;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Synthetic LTNF, LT-15.
 XX
 KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.
 XX
 PN WO2003060471-A2.
 XX

XX WO2003060471-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 14-JAN-2003; 2003WO-US001044.
 XX
 PR 14-JAN-2002; 2002US-00047945.
 XX
 XX (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.
 XX
 PI Lipps BV, Lipps FW;
 XX
 XX WPI; 2003-636703/60.
 DR
 XX Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 PT
 XX Claim 3; Page 3; 24pp; English.
 PS
 XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IgE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 54; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTPPL 10
 Db 1 LKAMDPTPPL 10
 |||||
 RESULT 8
 ABB80227
 ID ABB80227 standard; peptide; 9 AA.
 XX
 AC ABB80227;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Synthetic LTNF, LT-9.
 XX
 KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.
 XX
 PN WO2003060471-A2.
 XX


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PD 24-JUL-2003.
XX
XX
XX 14-JAN-2003; 2003WO-US001044.
XX
XX
XX 14-JAN-2002; 2002US-00047945.
XX
XX (LIPPP/) LIPPS B V.
XX (LIPPP/) LIPPS F W.
XX
XX Lipps BV, Lipps FW;
XX
XX WPI; 2003-636703/60.
XX
XX Assaying a human endogenous protein (e.g. IgG, nerve growth factor,
XX insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
XX asthma or diabetes, by employing an ELISA on a saliva sample from a
XX patient.
XX
XX Claim 7; Page 4; 24pp; English.
XX
XX The sequences given in ABB80222-28 represent lethal toxin neutralising
XX factor (LTNF) peptides which may be used for reducing elevated levels of
XX serum proteins selected from immunoglobulin E (IgE), nerve growth factor
XX (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
XX particular, the methods of the invention are useful for diagnosing and
XX treating conditions with elevated serum IgE levels, e.g. asthma,
XX diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid
XX arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
XX Addison's disease or Hodgkin's disease) or depression. The efficacy of
XX the protein may be monitored by assaying a human endogenous protein by
XX performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
XX collection using an anti-serum that is specific for the protein. Saliva
XX collection is relatively non-invasive when compared to blood collection
XX for serum. Saliva can be centrifuged immediately, whereas blood requires
XX clotting time before centrifugation to separate serum. Saliva proteins
XX can be assayed by a simple ELISA test, whereas an assay of proteins from
XX serum requires a more complicated sandwich type ELISA
XX
XX Sequence 9 AA;
XX
XX Query Match 92.6%; Score 50; DB 7; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 LKAMDPTPP 9
XX |||||
XX Db 1 LKAMDPTPP 9
XX
XX RESULT 9
XX ABB80228
XX ID ABB80228 standard; peptide; 8 AA.
XX
XX AC ABB80228;
XX
XX DT 06-NOV-2003 (first entry)
XX
XX DE Synthetic LTNF, LT-8.
XX
XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
XX IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
XX ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematous;
XX SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
XX Graves' disease; Addison's disease; Hodgkin's disease; depression;
XX saliva; ELISA.
XX
XX OS Synthetic.
XX
XX PN WO2003060471-A2.
XX
XX 24-JUL-2003.
XX
XX 14-JAN-2003; 2003WO-US001044.
XX

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XX 14-JAN-2002; 2002US-00047945.
XX
XX (LIPPP/) LIPPS B V.
XX (LIPPP/) LIPPS F W.
XX
XX Lipps BV, Lipps FW;
XX
XX WPI; 2003-636703/60.
XX
XX Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
XX insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
XX asthma or diabetes, by employing an ELISA on a saliva sample from a
XX patient.
XX
XX Claim 7; Page 4; 24pp; English.
XX
XX The sequences given in ABB80222-28 represent lethal toxin neutralising
XX factor (LTNF) peptides which may be used for reducing elevated levels of
XX serum proteins selected from immunoglobulin E (IgE), nerve growth factor
XX (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
XX particular, the methods of the invention are useful for diagnosing and
XX treating conditions with elevated serum IgE levels, e.g. asthma,
XX diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid
XX arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
XX Addison's disease or Hodgkin's disease) or depression. The efficacy of
XX the protein may be monitored by assaying a human endogenous protein by
XX performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
XX sample using an anti-serum that is specific for the protein. Saliva
XX collection is relatively non-invasive when compared to blood collection
XX for serum. Saliva can be centrifuged immediately, whereas blood requires
XX clotting time before centrifugation to separate serum. Saliva proteins
XX can be assayed by a simple ELISA test, whereas an assay of proteins from
XX serum requires a more complicated sandwich type ELISA
XX
XX Sequence 8 AA;
XX
XX Query Match 79.6%; Score 43; DB 7; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 LKAMDPTP 8
XX |||||
XX Db 1 LKAMDPTP 8
XX
XX RESULT 10
XX AA002179
XX ID AA002179 standard; protein; 94 AA.
XX
XX AC AA002179;
XX
XX DT 06-NOV-2001 (first entry)
XX
XX DE Human polypeptide SEQ ID NO 16071.
XX
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorders; arthritis; inflammation.
XX
XX OS Homo sapiens.
XX
XX PN WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US004927.
XX
XX 28-FEB-2000; 2000US-00515126.
XX
XX 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
XX

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XX Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-514838/56.
 DR N-PSDB; AAI82110.
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 PT Claim 20; SEQ ID NO 16071; 1399pp + Sequence Listing; English.
 XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 94' AA;
 SQ

Query Match 77.8%; Score 42; DB 4; Length 94;
 Best Local Similarity 77.8%; Pred. No. 28;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTTP 9
 Db 48 LKSQDPTTP 56
 ||:|||||

RESULT 11
 ABB58900
 ID ABB58900 standard; protein; 165 AA.
 AC ABB58900;
 XX 26-MAR-2002 (first entry)
 XX Drosophila melanogaster polypeptide SEQ ID NO 3492.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical.
 KW Drosophila melanogaster.
 XX WO200171042-A2.
 PN 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US009231.
 PF 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 DR N-PSDB; ABL03003.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX Disclosure; SEQ ID NO 3492; 21pp + Sequence Listing; English.
 PS
 XX

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 165 AA;
 SQ

Query Match 75.9%; Score 41; DB 4; Length 165;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPTPPL 10
 Db 1 MDPTPPL 7
 |||||

RESULT 12
 AAB59012
 ID AAB59012 standard; protein; 459 AA.
 XX AAB59012;
 AC AAB59012;
 XX 27-MAR-2001 (first entry)
 XX Breast and ovarian cancer associated antigen protein sequence SEQ ID 720.
 DE Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
 KW neurotropic; neuroprotective; antiviral; antiallergic; hepatotrophic;
 KW antidiabetic; antiinflammatory; antitumor; vulnery; anticonvulsant;
 KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease.
 XX Homo sapiens.
 OS WO200055173-A1.
 PN 21-SEP-2000.
 XX 08-MAR-2000; 2000WO-US005881.
 PF 12-MAR-1999; 99US-0124270P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Ruben SM;
 PI WPI; 2000-611515/58.
 DR N-PSDB; AAF21915.
 XX New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention, treatment
 PT and diagnosis of cancer, immune disorders, cardiovascular disorders and
 PT neurological diseases.
 XX Claim 11; Page 1174-1176; 1299pp; English.
 PS Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic; immunosuppressive; neurotropic;
 CC neuroprotective; antiviral; antiallergic; hepatotrophic; antidiabetic;

CC antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
 CC antifungal; antiparasitic and cardiant activity. The polynucleotide and
 CC protein sequences are used in the diagnosis of cancer, particularly
 CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
 CC and agonists may also be used in the diagnosis, prevention and treatment
 CC of immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC cardiovascular disorders such as myocardial ischaemia; wound healing;
 CC neurological diseases such as cerebral anoxia and epilepsy; and
 CC infectious diseases
 XX
 SQ Sequence 459 AA;

Query Match 72.2%; Score 39; DB 3; Length 459;
 Best Local Similarity 66.7%; Pred. No. 4.3e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTPP 9
 Db 346 LRSQDPTPP 354
 :: |||||

RESULT 13

ABM82174
 ID ABM82174 standard; protein; 754 AA.

XX AC ABM82174;

DT 18-NOV-2004 (first entry)

XX Tumour-associated antigenic target (TAT) polypeptide PRO83096, SEQ:5611.

XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 XX tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic.

XX Homo sapiens.

XX WO2004030615-A2.

XX 15-APR-2004.

XX 29-SEP-2003; 2003WO-US028547.

XX 02-OCT-2002; 2002US-0414971P.

XX (GETH) GENENTECH INC.

XX Wu TD, Zhang Z, Zhou Y;

XX WPI; 2004-347921/32.

XX N-PSDB; ACN40680.

PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.

XX Claim 12; SEQ ID NO 5611; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic

CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT polypeptide of the invention
 XX

SQ Sequence 754 AA;

Query Match 72.2%; Score 39; DB 8; Length 754;
 Best Local Similarity 66.7%; Pred. No. 7.1e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTPP 9
 Db 641 LRSQDPTPP 649
 :: |||||

RESULT 14

ADS88328
 ID ADS88328 standard; protein; 754 AA.

XX AC ADS88328;

DT 18-NOV-2004 (first entry)

XX Human protein of a TNF-alpha signalling pathway protein complex Seq 183.

XX Protein complex; tumour necrosis factor-alpha signalling pathway;
 KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
 KW inflammatory bowel disease; infectious disease; septic shock;
 KW bacterial infection; neurological disease; stroke-induced inflammation;
 KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
 KW antirheumatic; cytostatic; antibacterial; gene therapy; human.

XX Homo sapiens.

XX WO2004035783-A2.

XX 29-APR-2004.

XX 24-SEP-2003; 2003WO-EP050655.

XX 26-SEP-2002; 2002EP-00021809.

XX 10-FEB-2003; 2003EP-00100274.

XX (CELL-) CELLZONE AG.

XX Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
 XX Superti-Furga G, Kruse U;

XX WPI; 2004-348460/32.

XX New protein complex comprising at least one first and second protein of
 PT the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
 PT diagnosing or treating inflammation, neurological diseases, infectious
 PT diseases or cancer.

XX Example; SEQ ID NO 183; 1980pp; English.

XX This invention relates to novel protein complexes of the tumour necrosis
 CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
 CC methods for preparing these complexes comprising at least two component
 CC proteins, as well as screening methods to identify modulators of the
 CC pathway, which include antibodies, agonists and antagonists thereof. The
 CC present invention describes a protein complex and kit that are useful for
 CC diagnosing, prognosing or treating chronic inflammatory diseases such as

CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
CC such as septic shock and bacterial infections; neurological diseases such
CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
CC cancer. Accordingly, these complexes can be used for the development of
CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
CC antirheumatic, cytostatic and antibacterial activities and can be used
CC for gene therapy purposes. In particular, the invention further provides
CC siRNA-oligonucleotides useful for inhibiting protein expression for in
CC vitro or cell culture assays. This polypeptide is a human protein that
CC can be used in combination with other proteins provided in the
CC specification to form novel complexes of the TNF-alpha signalling pathway
CC of the invention.

XX Sequence 754 AA;

Query Match 72.2%; Score 39; DB 8; Length 754;
Best Local Similarity 66.7%; Pred. No. 7.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels -0; Gaps 0;

QY 1 LKXMDPTTP 9
Db 641 LRSQDPTTP 649

RESULT 15

AA085892
ID AA085892 standard; protein; 78 AA.

XX
AC AA085892;

DT 07-NOV-2001 (first entry)

DE Human immune/haematopoietic antigen SEQ ID NO:13485.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.

XX Homo sapiens.

XX WO200157182-A2.

XX 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 20-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0228279P.
PR 22-AUG-2000; 2000US-0228681P.
PR 22-AUG-2000; 2000US-0228688P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
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PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
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PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 05-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-483426/52.

XX N-PSDB; AAK58673.

XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.

XX Claim 11; SEQ ID NO 13485; 3071pp + Sequence Listing; English.

XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention

XX SQ Sequence 78 AA;

Query Match 70.4%; Score 38; DB 4; Length 78;

Best Local Similarity 70.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LKAMDPTPPL 10

Db S LPALPPTPPL 14

Search completed: May 26, 2005, 18:36:48
Job time : 90 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:43:39 ; Search time 65.6 Seconds
(without alignments)
52.587 Million cell updates/sec

Title: US-10-047-945-1
Perfect score: 54
Sequence: 1 LKAMDPTPPL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	54	100.0	11	14	US-10-047-945-5
3	54	100.0	12	14	US-10-047-945-4
4	54	100.0	15	14	US-10-047-945-2
5	50	92.6	9	14	US-10-047-945-6
6	43	79.6	8	14	US-10-047-945-7
7	41	75.9	80	15	US-10-424-599-253125
8	41	75.9	148	16	US-10-437-963-133945
9	39	72.2	169	16	US-10-437-963-162813
10	39	72.2	206	16	US-10-437-963-162816
11	39	72.2	459	9	US-09-925-298-720
12	39	72.2	459	14	US-10-102-806-720
13	38	70.4	75	16	US-10-767-701-51220

14	38	70.4	132	16	US-10-437-963-138037	Sequence 138037,
15	38	70.4	369	17	US-10-732-923-1996	Sequence 1996, Ap
16	38	70.4	369	17	US-10-732-923-1997	Sequence 1997, Ap
17	37	68.5	15	14	US-10-161-791-444	Sequence 444, App
18	37	68.5	54	15	US-10-424-599-158162	Sequence 158162,
19	37	68.5	67	15	US-10-424-599-273019	Sequence 273019,
20	37	68.5	210	9	US-09-071-035-232	Sequence 232, App
21	37	68.5	210	14	US-10-206-576-232	Sequence 232, App
22	37	68.5	210	17	US-10-912-362-232	Sequence 232, App
23	37	68.5	244	16	US-10-437-963-179361	Sequence 179361,
24	37	68.5	256	9	US-09-071-035-230	Sequence 230, App
25	37	68.5	256	14	US-10-206-576-230	Sequence 230, App
26	37	68.5	256	17	US-10-912-362-230	Sequence 230, App
27	37	68.5	270	15	US-10-282-122A-57118	Sequence 57118, A
28	37	68.5	285	15	US-10-282-122A-56870	Sequence 56870, A
29	37	68.5	367	16	US-10-437-963-146546	Sequence 146546,
30	37	68.5	481	15	US-10-369-493-7817	Sequence 7817, Ap
31	37	68.5	736	15	US-10-425-114-68941	Sequence 68941, A
32	37	68.5	1529	17	US-10-732-923-8762	Sequence 8762, Ap
33	36	66.7	34	16	US-10-437-963-127940	Sequence 127940,
34	36	66.7	126	16	US-10-437-963-135430	Sequence 135430,
35	36	66.7	139	15	US-10-424-599-280103	Sequence 280103,
36	36	66.7	204	16	US-10-437-963-190433	Sequence 190433,
37	36	66.7	222	15	US-10-335-977-8979	Sequence 8979, Ap
38	36	66.7	231	16	US-10-767-701-56593	Sequence 56593, A
39	36	66.7	412	15	US-10-282-122A-62510	Sequence 62510, A
40	36	66.7	431	15	US-10-369-493-6365	Sequence 6365, Ap
41	36	66.7	460	15	US-10-282-122A-64604	Sequence 64604, A
42	36	66.7	575	15	US-10-424-599-166372	Sequence 166372,
43	36	66.7	577	15	US-10-104-047-3148	Sequence 3148, Ap
44	36	66.7	646	15	US-10-282-122A-59738	Sequence 59738, A
45	36	66.7	920	16	US-10-437-963-181405	Sequence 181405,

ALIGNMENTS

RESULT 1
US-10-047-945-1
; Sequence 1, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: (IGF) IMPLICATED DISORDERS
; FILE REFERENCE: FWPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED.
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-1

Query Match 100.0%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10
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Db 1 LKAMDPTPPL 10

RESULT 2
US-10-047-945-5
; Sequence 5, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.
US-10-047-945-5

Query Match 100.0%; Score 54; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.062; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDTPPL 10
| | | | | | | |
Db 1 LKAMDTPPL 10

RESULT 3
US-10-047-945-4
; Sequence 4, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.
US-10-047-945-4

Query Match 100.0%; Score 54; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.068; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDTPPL 10
| | | | | | | |
Db 1 LKAMDTPPL 10

RESULT 4
US-10-047-945-2
; Sequence 2, Application US/10047945

; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-2

Query Match 100.0%; Score 54; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.085; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDTPPL 10
| | | | | | | |
Db 1 LKAMDTPPL 10

RESULT 5
US-10-047-945-6
; Sequence 6, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.
US-10-047-945-6

Query Match 92.6%; Score 50; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDTPP 9
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Db 1 LKAMDTPP 9

RESULT 6
US-10-047-945-7
; Sequence 7, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:

; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IGE)IMPLICATED DISORDERS
; FILE REFERENCE: FWPAT0150S
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
US-10-047-945-7

Query Match 79.6%; Score 43; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
| | | | |
Db 1 LKAMDPTP 8

RESULT 7
US-10-424-599-253125
; Sequence 253125, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 253125
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_70598C.1.pep
US-10-424-599-253125

Query Match 75.9%; Score 41; DB 15; Length 80;
Best Local Similarity 70.0%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10
| | | | |
Db 62 LKGTDPPTPV 71

RESULT 8
US-10-437-963-133945
; Sequence 133945, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133945
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(148)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35767C.1.pep
US-10-437-963-133945

Query Match 75.9%; Score 41; DB 16; Length 148;
Best Local Similarity 70.0%; Pred. No. 83;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10
| | | | |
Db 42 LRAREPTPPL 51

RESULT 9
US-10-437-963-162813
; Sequence 162813, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162813
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(169)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61869C.1.pep
US-10-437-963-162813

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Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10
| | | | |
Db 61 LSSLDPSPL 70

RESULT 10
US-10-437-963-162816
; Sequence 162816, Application US/10437963
; Publication No. US20040123343A1

GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162816
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(206)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61871C.1.pgp
US-10-437-963-162816

Query Match 72.2%; Score 39; DB 16; Length 206;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDTPPL 10
| : : : : :
Db 67 LSSLDPSPEL 76

RESULT 11
US-09-925-298-720
; Sequence 720, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 720
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-298-720

Query Match 72.2%; Score 39; DB 9; Length 459;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDTPPP 9
| : : : : :
Db 346 LRSQDTPPP 354

RESULT 12
US-10-102-806-720

; Sequence 720, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103PIC1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 720
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-720

Query Match 72.2%; Score 39; DB 14; Length 459;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDTPPP 9
| : : : : :
Db 346 LRSQDTPPP 354

RESULT 13
US-10-767-701-51220
; Sequence 51220, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 51220
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3481-060-Q6-K1-D12.pgp
US-10-767-701-51220

Query Match 70.4%; Score 38; DB 16; Length 75;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDTPPP 9
| : : : : :
Db 2 LKYMPPPPP 10

RESULT 14
US-10-437-963-138037
; Sequence 138037, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

```

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 138037
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_39462C.1.pap
US-10-437-963-138037

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Query Match      70.4%; Score 38; DB 16; Length 132;
Best Local Similarity 60.0%; Pred. NO. 2.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 LKANDTPPL 10
      : : |||||
Db      1 MPSQDTPPL 10

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RESULT 15
US-10-732-923-1996
; Sequence 1996, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1996
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-732-923-1996

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Query Match      70.4%; Score 38; DB 17; Length 369;
Best Local Similarity 75.0%; Pred. NO. 5.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 KAMDTPP 9
      : : |||||
Db      59 KAVEPTPP 66

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Search completed: May 26, 2005, 19:16:33
Job time : 71.6 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2005, 18:29:58 ; Search time 22.8 Seconds
(without alignments)
32.741 Million cell updates/sec

Title: US-10-047-945-1

Perfect score: 54

Sequence: 1 LKAWDPTPL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	10	1	US-08-657-163A-2
2	54	100.0	15	1	US-08-310-340A-1
3	54	100.0	15	1	US-08-657-163A-1
4	41	75.9	253	4	US-09-270-767-43223
5	39	72.2	72	4	US-09-949-016-8760
6	38	70.4	267	2	US-07-857-224B-42
7	37	68.5	15	3	US-08-602-939A-444
8	37	68.5	15	4	US-09-500-124-444
9	37	68.5	210	4	US-09-071-035-232
10	37	68.5	256	4	US-09-071-035-230
11	37	68.5	291	4	US-09-134-000C-6676
12	37	68.5	306	4	US-09-489-039A-13855
13	36	66.7	323	4	US-09-489-039A-13855
14	36	66.7	338	4	US-09-248-796A-20624
15	35	64.8	27	4	US-09-270-767-57016
16	35	64.8	206	4	US-09-538-092-166
17	35	64.8	315	1	US-08-571-758-12
18	35	64.8	315	1	US-08-909-984A-12
19	35	64.8	315	1	US-08-909-983-12
20	35	64.8	323	4	US-09-248-796A-16328
21	35	64.8	346	1	US-08-276-151-5
22	35	64.8	405	4	US-09-489-039A-9126
23	35	64.8	648	1	US-08-276-151-2
24	35	64.8	648	1	US-08-185-282-1
25	35	64.8	648	1	US-08-185-282-2
26	35	64.8	648	1	US-08-185-282-3
27	35	64.8	648	1	US-08-185-282-4

28	35	64.8	648	1	US-08-185-282-5
29	35	64.8	648	1	US-08-185-282-12
30	35	64.8	648	2	US-08-886-751A-6
31	35	64.8	648	3	US-09-209-668-13
32	35	64.8	648	3	US-08-971-207-1
33	35	64.8	648	4	US-08-207-954-3
34	35	64.8	657	4	US-09-653-465B-2
35	35	64.8	825	4	US-10-210-428-1
36	35	64.8	825	4	US-10-237-551-161
37	35	64.8	826	4	US-09-894-998A-47
38	35	64.8	826	4	US-10-237-551-47
39	35	64.8	1068	1	US-08-537-210A-2
40	35	64.8	1068	3	US-09-113-825-2
41	35	64.8	1078	1	US-08-264-534-32
42	35	64.8	1078	1	US-08-083-590A-11
43	35	64.8	1078	1	US-08-465-500-32
44	35	64.8	1078	2	US-08-346-128-32
45	35	64.8	1078	3	US-08-532-384-11

ALIGNMENTS

RESULT 1

US-08-657-163A-2

; Sequence 2, Application US/08657163A

; Patent No. 5744449

; GENERAL INFORMATION:

; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS

; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND

; TITLE OF INVENTION: SYNTHETIC LIPIDS AND THEIR

; TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BINIE V. LIPPS

; STREET: 4509 MIMOSA DR.

; CITY: BELLAIRE

; STATE: TEXAS

; COUNTRY: USA

; ZIP: 77401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB

; COMPUTER: IBM COMPATIBLE

; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1

; SOFTWARE: MS WORD 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/657,163A

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/310,340

; FILING DATE: 22 SEPTEMBER 1994

; CLASSIFICATION: 514

; APPLICATION NUMBER: 08/058,387

; FILING DATE: 10 MAY 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: JOHN R. CASPERSON

; REGISTRATION NUMBER: 28,198

; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 713-482-2961

; TELEFAX: 713-663-7290

; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10

; TYPE: AMINO ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N

ORIGINAL SOURCE: SYNTHETIC
US-08-657-163A-2

Query Match 100.0%; Score 54; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDTPPL 10
| | | | | | | | | |
Db 1 LKAMDTPPL 10

RESULT 2
US-08-310-340A-1
; Sequence 1, Application US/08310340A
; Patent No. 5576297
; GENERAL INFORMATION:
; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
; TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR
; TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BINIE V. LIPPS
; STREET: 4509 MIMOSA DR.
; CITY: BELLAIRE
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
; SOFTWARE: MS WORD 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,340A
; FILING DATE: 22 SEPTEMBER 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: 08/058, 387
; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-723-6845
; TELEFAX: 713-663-7290
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; LENGTH: 15
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N
; ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
; ORGANISM: DIDELPHIS VIRGINIANA
; STRAIN: WILD
; INDIVIDUAL ISOLATE: TEXAS WILD
; DEVELOPMENTAL STAGE: ADULT
; HAPLOTYPE:
; TISSUE TYPE: BLOOD
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
; LIBRARY:
; CLONE:
; PUBLICATION INFORMATION:

AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
VOLUME: SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
US-08-310-340A-1

Query Match 100.0%; Score 54; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDTPPL 10
| | | | | | | | | |
Db 1 LKAMDTPPL 10

RESULT 3
US-08-657-163A-1
; Sequence 1, Application US/08657163A
; Patent No. 5744449
; GENERAL INFORMATION:
; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
; TITLE OF INVENTION: SYNTHETIC LTNFS AND THEIR
; TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BINIE V. LIPPS
; STREET: 4509 MIMOSA DR.
; CITY: BELLAIRE
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
; SOFTWARE: MS WORD 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,163A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,340
; FILING DATE: 22 SEPTEMBER 1994
; CLASSIFICATION: 514
; APPLICATION NUMBER: 08/058,387
; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN R. CASPERSON
; REGISTRATION NUMBER: 28,198
; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-482-2961
; TELEFAX: 713-663-7290
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N
; ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
; ORGANISM: DIDELPHIS VIRGINIANA

;
; STRAIN: WILD
; INDIVIDUAL ISOLATE: TEXAS WILD
; DEVELOPMENTAL STAGE: ADULT
; RAPLOTYPE:
; TISSUE TYPE: BLOOD
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1;
; LIBRARY:
; CLONE:
; PUBLICATION INFORMATION:
; AUTHORS: JONAS PERALES, ET AL.
; TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
; JOURNAL: INTERNATIONAL SOCIETY ON
; JOURNAL: TOXICOLOGY
; VOLUME: 10TH WORLD CONGRESS ON ANIMAL
; VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
; ISSUE: PROGRAMME AND ABSTRACTS
; PAGES: 104
; DATE: 3-8 NOV 1991
; US-08-657-163A-1

Query Match 100.0%; Score 54; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPL 10
| | | | |
Db 1 LKAMDPTPL 10

RESULT 4
US-09-270-767-43223
; Sequence 43223, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 43223
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43223

Query Match 75.9%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDPTPL 10
| | | | |
Db 43 MDPTPL 49

RESULT 5
US-09-949-016-8760
; Sequence 8760, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8760
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8760

Query Match 72.2%; Score 39; DB 4; Length 72;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTTP 9
| | | | |
Db 61 RTMDPTTP 68

RESULT 6
US-07-857-224B-42
; Sequence 42, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
; TELEX: none

INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 267
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
FEATURE: Protein kinase; Table 8 Column 48
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-52
DATE: 1988
US-07-857-224B-42

Query Match 70.4%; Score 38; DB 2; Length 267;
 Best Local Similarity 70.0%; Pred. No. 67;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDTPPL 10
 ||:|||||
 Db 31 LKVDTPPL 40

RESULT 7

US-08-602-999A-444
 ; Sequence 444, Application US/08602999A
 ; Patent No. 6184205

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
 APPLICANT: KAY, Brian K.
 APPLICANT: THORN, Judith M.
 APPLICANT: QUILLIAM, Lawrence A.
 APPLICANT: DER, Channing J.
 APPLICANT: FOWLKES, Dana M.
 APPLICANT: RIDER, James E.
 TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 TITLE OF INVENTION: ISOLATING AND USING SAME
 NUMBER OF SEQUENCES: 467
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/602,999A
 FILING DATE: 16-FEB-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 1101-202
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 444:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide

US-08-602-999A-444

Query Match 68.5%; Score 37; DB 3; Length 15;
 Best Local Similarity 66.7%; Pred. No. 4.5;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMDTPPL 10
 ||:|||||
 Db 5 RALPPTPL 13

RESULT 8

US-09-500-124-444
 ; Sequence 444, Application US/09500124
 ; Patent No. 6432920

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
 APPLICANT: KAY, Brian K.
 APPLICANT: THORN, Judith M.

APPLICANT: QUILLIAM, Lawrence A.
 APPLICANT: DER, Channing J.
 APPLICANT: FOWLKES, Dana M.
 APPLICANT: RIDER, James E.
 TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 TITLE OF INVENTION: ISOLATING AND USING SAME
 NUMBER OF SEQUENCES: 467
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/500,124
 FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/602,999
 FILING DATE: 16-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 1101-202
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 444:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide

US-09-500-124-444

Query Match 68.5%; Score 37; DB 4; Length 15;
 Best Local Similarity 66.7%; Pred. No. 4.5;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMDTPPL 10
 ||:|||||
 Db 5 RALPPTPL 13

RESULT 9

US-09-071-035-232
 ; Sequence 232, Application US/09071035
 ; Patent No. 6448043

GENERAL INFORMATION:

APPLICANT: Gil H. Choi
 TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
 NUMBER OF SEQUENCES: 496
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/071,035

;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: A. Anders Brookes
;; REGISTRATION NUMBER: 36,373
;; REFERENCE/DOCKET NUMBER: PB369P2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8512
;; INFORMATION FOR SEQ ID NO: 232:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 210 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-071-035-232

Query Match 68.5%; Score 37; DB 4; Length 210;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KAMPTPPL 10
| | | | |
Db 24 KPTDTPPI 32

RESULT 10
US-09-071-035-230
; Sequence 230, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 230:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-230

Query Match 68.5%; Score 37; DB 4; Length 256;
Best Local Similarity 66.7%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KAMPTPPL 10
| | | | |
Db 50 KPTDTPPI 58

RESULT 11
US-09-134-000C-6676
; Sequence 6676, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6676
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6676

Query Match 68.5%; Score 37; DB 4; Length 291;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KAMPTPPL 10
| | | | |
Db 70 KPTDTPPI 78

RESULT 12
US-09-134-000C-6583
; Sequence 6583, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6583
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6583

Query Match 68.5%; Score 37; DB 4; Length 306;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KAMPTPPL 10
| | | | |
Db 70 KPTDTPPI 78

RESULT 13
US-09-489-039A-13655
; Sequence 13655, Application US/09489039A
; Patent No. 6610836

; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13655
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13655

Query Match 66.7%; Score 36; DB 4; Length 323;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPP 9
Db 6 LKAMDALPP 14

RESULT 14
US-09-248-796A-20624
; Sequence 20624, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20624
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20624

Query Match 66.7%; Score 36; DB 4; Length 338;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMDPTPPL 10
Db 88 KAKDPTDPL 96

RESULT 15
US-09-270-767-57016
; Sequence 57016, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57016
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57016

Query Match 64.8%; Score 35; DB 4; Length 27;
Best Local Similarity 55.6%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 LKAMDPTPP 9
Db 19 LRPLDPSPP 27
Search completed: May 26, 2005, 19:08:37
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:26:23 ; Search time 23.7 Seconds
(without alignments)
60.897 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKAMDTPPLWKTE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	75.0	237	2 A42013	alpha-1-B-glycopro
2	46	54.8	1213	2 A54063	TATA-binding prote
3	44	52.4	695	2 E75099	hypothetical prote
4	44	52.4	777	2 T38769	hypothetical prote
5	44	52.4	1327	2 T09402	immunoglobulin-lik
6	43	51.2	341	2 AB0644	probable glycosyl
7	43	51.2	687	2 D86314	hypothetical prote
8	43	51.2	932	1 A31898	hypothetical prote
9	42	50.0	115	2 D81717	conserved hypotet
10	42	50.0	398	2 AB1719	aspartate transami
11	42	50.0	453	2 T04646	major structural n
12	42	50.0	564	1 VHXPWV	fasciclin I precur
13	42	50.0	662	2 A29900	ribosomal protein
14	41	48.8	151	1 S30146	myocyte enhancer f
15	41	48.8	339	2 JC5882	myocyte enhancer f
16	41	48.8	349	2 JC5881	two-component sens
17	41	48.8	411	2 AE2152	probable acyl-CoA
18	41	48.8	707	2 F86925	antibiotic Pep5 b
19	41	48.8	967	2 S58360	exodeoxyribonucle
20	41	48.8	975	2 T03004	hypothetical prote
21	41	48.8	1172	2 T00065	probable DNA (cyto
22	41	48.8	1559	2 T07757	C4 protein - tomat
23	40	47.6	97	2 S59888	microfilament shea
24	40	47.6	205	2 S26854	proline-rich shea
25	40	47.6	205	2 A40525	virC-region hypoth
26	40	47.6	209	2 B40049	type III secretion
27	40	47.6	209	2 T43565	hypothetical prote
28	40	47.6	210	2 S21428	two-component resp
29	40	47.6	225	2 C70045	

30 40 47.6 231 2 F69977 two-component resp
31 40 47.6 309 2 H72626 probable 2-oxoacid
32 40 47.6 337 2 A97084 uncharacterized pr
33 40 47.6 406 2 C83867 Xaa-Pro dipeptidas
34 40 47.6 422 2 D86446 hypothetical prote
35 40 47.6 560 2 T02404 probable beta-gluc
36 40 47.6 609 2 S65208 probable membrane
37 40 47.6 1184 2 D86387 hypothetical prote P
38 40 47.6 1215 2 E70614 mucin MUC5B, trach
39 40 47.6 3570 2 T45025 dprA protein [impo
40 39.5 47.0 365 2 F87552 probable serine/th
41 39.5 47.0 631 2 A57286 hypothetical prote
42 39 46.4 242 2 AD1528
43 39 46.4 256 1 WMBEPN
44 39 46.4 258 2 T23957
45 39 46.4 268 2 S31010 gene 65 protein -

ALIGNMENTS

RESULT 1

A42013

Alpha-1-B-glycoprotein - North American opossum (fragments)

C:Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)
C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004

C:Accession: A42013

R:Cataneese, J.J.; Kress, L.F.

Biochemistry 31, 410-418, 1992

A:Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hum

A:Reference number: A42013; MUID:92118834; PMID:1731898

A:Accession: A42013

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-237 <CAT>

A:Cross-references: UNIPROT:Q28359; GB:J05356

C:Keywords: glycoprotein

Query Match 75.0%; Score 63; DB 2; Length 237;

Best Local Similarity 80.0%; Pred. No. 0.0095;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDTPPLWKTE 15

||||| :|||:|

Db 1 LKAMDTPPLWKTE 15

RESULT 2

A54063

TATA-binding protein-associated factor II - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004

C:Accession: A54063

R:Verrijzer, C.P.; Yokomori, K.; Chen, J.L.; Tjian, R.

Science 264, 933-941, 1994

A:Title: Drosophila TAF-II 150: similarity to yeast Gene TSM-1 and specific binding to c

A:Reference number: A54063; MUID:94233377; PMID:8178153

A:Accession: A54063

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-1213 <VER>

A:Cross-references: UNIPROT:Q24325; GB:X79243; NID:G541664; PIDN:CAA55830.1; PID:G541665

C:Genetics:

A:Gene: FlyBase:Taf150

A:Cross-references: FlyBase:FBgn0011836

Query Match 54.8%; Score 46; DB 2; Length 1213;

Best Local Similarity 53.3%; Pred. No. 32;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LKAMDTPPLWKTE 15

||||| :|||:|

Db 620 LSAMDDSPVLWRLD 634

A;Cross-references: UNIPROT:Q9LMT8; GB:AE005172; NID:g9665069; PIDN:AAF97271.1; GSPDB:GN
 C;Genetics:
 A;Map position: 1
 C;Superfamily: homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 51.2%; Score 43; DB 2; Length 687;
 Best Local Similarity 46.7%; Pred. No. 52;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LKMDPTPLWIKTE 15
 | : |||||
 Db 225 LRLQTNELPLWIKTD 239

RESULT 8
 A31898
 hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) - sea urchin (Strongylocentrotus purpuratus)
 C;Species: Strongylocentrotus purpuratus (purple urchin)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: A31898; A28367
 R;Woodward, H.D.; Allen, J.M.C.; Lennarz, W.J.
 J. Biol. Chem. 263, 18411-18418, 1988
 A;Title: 3-hydroxy-3-methylglutaryl-coenzyme A reductase of the sea urchin embryo. Deduced from complementary DNA
 A;Reference number: A31898; MUID:89054023; PMID:3192541
 A;Accession: A31898
 A;Molecule type: mRNA
 A;Residues: 1-932 <WOO>
 A;Cross-references: UNIPROT:P16393; GB:J04200; NID:g161522; PIDN:AAA30060.1; PID:g161523
 A;Note: the authors rearranged portions of the coding region in Figure 2, and the above submitted to GenBank

A;Note: the authors translated the codon GCA for residue 805 as Glu
 R;Woodward, H.D.; Allen, J.M.C.; Lennarz, W.J.
 J. Biol. Chem. 263, 2513-2517, 1988
 A;Title: 3-hydroxy-3-methylglutaryl coenzyme A reductase in the sea urchin embryo is dev
 A;Reference number: A28367; MUID:88115403; PMID:3276692
 A;Accession: A28367
 A;Molecule type: mRNA
 A;Residues: 689-735 <W02>
 C;Comment: This transmembrane glycoprotein of the endoplasmic reticulum is involved in t
 C;Superfamily: hydroxymethylglutaryl-CoA (HMG-CoA) reductase
 C;Keywords: cholesterol biosynthesis; coenzyme A; endoplasmic reticulum; glycoprotein; N
 F;279,850,886,930/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.2%; Score 43; DB 1; Length 932;
 Best Local Similarity 70.0%; Pred. No. 73;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KAMDPTPLW 11
 | : |||||
 Db 298 KKIDPTPLW 307

RESULT 9
 D71194
 hypothetical protein PH1828 - Pyrococcus horikoshii
 C;Species: Pyrococcus horikoshii
 C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
 C;Accession: D71194
 R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A;Reference number: A71000; MUID:98344137; PMID:9679194
 A;Accession: D71194
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-115 <KAW>
 A;Cross-references: UNIPROT:O59492; GB:AP000007; NID:g3236134; PIDN:BAA30947.1; PID:g325
 A;Experimental source: strain OT3
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C;Genetics:
 A;Gene: PH1828

Query Match 50.0%; Score 42; DB 2; Length 115;
 Best Local Similarity 66.7%; Pred. No. 10;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDPTPLWI 12
 | : |||||
 Db 89 ISPSPLWI 97

RESULT 10
 A81717
 conserved hypothetical protein TC0306 [imported] - Chlamydia muridarum (strain Nigg)
 C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: A81717
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Winn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 A;Accession: A81717
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-398 <TET>
 A;Cross-references: UNIPROT:Q9PL02; GB:AE002298; GB:AE002160; NID:g7190343; PIDN:AAF3917
 A;Experimental source: strain Nigg (MoPn)
 C;Genetics:
 A;Gene: TC0306
 C;Superfamily: Chlamydia trachomatis hypothetical protein CT036

Query Match 50.0%; Score 42; DB 2; Length 398;
 Best Local Similarity 77.8%; Pred. No. 41;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTPL 10
 | : |||||
 Db 309 KELDPTPL 317

RESULT 11
 T04646
 aspartate transaminase (EC 2.6.1.1) precursor, chloroplast - Arabidopsis thaliana
 N;Alternate names: aspartate aminotransferase; protein F10N7.200
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
 C;Accession: T04646; S5657; S47490
 R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X
 submitted to the Protein Sequence Database, March 1999
 A;Reference number: Z15263
 A;Accession: T04646
 A;Molecule type: DNA
 A;Residues: 1-453 <BEV>
 A;Cross-references: UNIPROT:P46248; EMBL:AL021636
 A;Experimental source: Cultivar Columbia; BAC clone F10N7
 R;Wilkie, S.E.; Roper, J.M.; Smith, A.G.; Warren, M.J.
 Plant Mol. Biol. 27, 1227-1233, 1995
 A;Title: Isolation, characterization and expression of a cDNA clone encoding plastid asp
 A;Reference number: S5657; MUID:95284373; PMID:7766905
 A;Accession: S5657
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-21 'NV', 24-453 <WIL>
 A;Cross-references: EMBL:X81026; NID:g531554; PIDN:CAA56932.1; PID:g531555
 C;Genetics:
 A;Gene: aat1
 A;Map position: 4
 A;Genome: nuclear
 A;Introns: 20/3; 37/3; 102/3; 115/3; 145/3; 182/1; 218/3; 266/3; 322/2; 410/3
 A;Note: F10N7.200
 C;Superfamily: aspartate aminotransferase
 C;Keywords: aminotransferase; chloroplast; phosphoprotein; pyridoxal phosphate
 F;298/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 50.0%; Score 42; DB 2; Length 453;
 Best Local Similarity 60.0%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPLWK 13
 : ||||| :
 Db 238 IDPTQWVK 247

RESULT 12
 VHXPMV
 major structural nucleoprotein - Machupo virus
 N:Alternate names: nucleocapsid protein
 C:Species: Machupo virus
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C:Accession: S18042
 R:Griffiths, C.; Wilson, S.M.; Clegg, J.C.S.
 A:Description: The EMBL Data Library, October 1991
 A:Reference number: S18042
 A:Accession: S18042
 A:Molecule type: genomic RNA
 A:Residues: 1-564 <GRI>
 A:Cross-references: UNIPROT:P26578; EMBL:X62616; NID:G60621; PID:G60622
 C:Genetics:
 A:Map position: segment S
 C:Superfamily: arenavirus major nucleoprotein
 C:Keywords: nucleocapsid; nucleoprotein

Query Match 50.0%; Score 42; DB 1; Length 564;
 Best Local Similarity 46.7%; Pred. No. 60;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWKTE 15
 : ||||| :
 Db 368 VKKLDPTNTLWLDIE 382

RESULT 13
 A29900
 fasciclin I precursor - American bird grasshopper
 C:Species: Schistocerca americana (American bird grasshopper)
 C:Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 09-Jul-2004
 C:Accession: A29900; A31817
 R:Zinn, K.; McAllister, L.; Goodman, C.S.
 Cell 53, 577-587, 1988
 A:Title: Sequence analysis and neuronal expression of fasciclin I in grasshopper and Drosophila
 A:Reference number: A29900; MUID:88223351; PMID:3370670
 A:Accession: A29900
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-662 <ZIN>
 A:Cross-references: UNIPROT:P10675; GB:M20544; GB:J03787; NID:g160846; PID:g160847
 R:Snow, P.M.; Zinn, K.; Harrelson, A.L.; McAllister, L.; Schilling, J.; Bastiani, M.J.;
 Proc. Natl. Acad. Sci. U.S.A. 85, 5291-5295, 1988
 A:Title: Characterization and cloning of fasciclin I and fasciclin II glycoproteins in Drosophila
 A:Reference number: A94202; MUID:88276943; PMID:2839842
 A:Accession: A31817
 A:Molecule type: mRNA
 A:Residues: 25-42 <SNO>
 A:Cross-references: EMBL:M20544; EMBL:J03787

Query Match 50.0%; Score 42; DB 2; Length 662;
 Best Local Similarity 58.3%; Pred. No. 72;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWI 12
 : ||||| :
 Db 104 LSELDGNPLWI 115

RESULT 14

S30146
 ribosomal protein S13, cytosolic - maize
 C:Species: Zea mays (maize)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: S30146
 R:Joanin, P.; Gigot, C.; Philipps, G.
 Plant Mol. Biol. 21, 701-704, 1993
 A:Title: cDNA nucleotide sequence and expression of a maize cytoplasmic ribosomal protein
 A:Reference number: S30146; MUID:93192530; PMID:8448368
 A:Accession: S30146
 A:Molecule type: mRNA
 A:Residues: 1-151 <JOA>
 A:Cross-references: UNIPROT:Q05761; EMBL:X62455; NID:G288058; PID:CAA44311.1; PID:G288058
 C:Superfamily: rat ribosomal protein S13; eubacterial ribosomal protein S15 homology
 C:Keywords: protein biosynthesis; ribosome
 F:2-151/Product: ribosomal protein S13 #status predicted <MAT>
 F:82-148/Domain: eubacterial ribosomal protein S15 homology <ES15>

Query Match 48.8%; Score 41; DB 1; Length 151;
 Best Local Similarity 75.0%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 TPPLWK 14
 : ||||| :
 Db 21 TPPTWLKT 28

RESULT 15
 JC5882
 myocyte enhancer factor 2B-2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Mar-1998 #sequence_revision 11-Mar-1998 #text_change 09-Jul-2004
 C:Accession: JC5882
 R:Morisaki, T.; Sermsuvitayawong, K.; Byun, S.H.; Matsuda, Y.; Hidaka, K.; Morisaki, H.;
 J. Biochem. 122, 939-946, 1997
 A:Title: Mouse Mef2b gene: Unique member of MEF2 gene family.
 A:Reference number: JC5881; MUID:98104045; PMID:9443808
 A:Accession: JC5882
 A:Molecule type: DNA
 A:Residues: 1-339 <MOR>
 A:Cross-references: UNIPROT:O55087; DDBJ:D87828
 C:Comment: This factor plays a differentiation of myocytes, including cardiomyocytes.
 C:Genetics:
 A:Gene: Mef2b
 A:Map position: 8
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRE>

Query Match 48.8%; Score 41; DB 2; Length 339;
 Best Local Similarity 61.5%; Pred. No. 50;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 AMDPTPLWKTE 15
 : ||||| :
 Db 281 ASPPTPPVSIKSE 293

Search completed: May 26, 2005, 18:44:46
 Job time : 26.7 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:18:07 ; Search time 114.6 Seconds
(without alignments)
67.026 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKAMDPTPLWKTE 15

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	17	2 Q9TR78	Q9tr78 didelphis m
2	84	100.0	291	1 DM43_DIDMR	P82957 didelphis m
3	75	89.3	140	2 Q8HZ75	Q8hz75 didelphis m
4	75	89.3	291	2 Q8HZ74	Q8hz74 didelphis m
5	63	75.0	314	2 Q8HYX5	Q8hyx5 didelphis m
6	52	61.9	504	2 Q8MIS3	Q8mi33 didelphis m
7	50	59.5	227	2 Q73ZB2	Q73zb2 mycobacteri
8	48	57.1	344	2 Q7MTQ9	Q7mtq9 porphyromon
9	47	56.0	51	2 Q8FNB0	Q8fnb0 corynebacte
10	47	56.0	351	1 Y4VJ_RH1SN	Q51218 rhizobium s
11	46	54.8	370	2 Q7QE78	Q7qe78 anopheles g
12	46	54.8	634	2 Q9VQP3	Q9vqp3 drosophila
13	46	54.8	854	2 Q9VQP4	Q9vqp4 drosophila
14	46	54.8	856	2 Q9GZ10	Q9gz10 drosophila
15	46	54.8	1017	2 Q7KU30	Q7ku30 drosophila
16	46	54.8	1221	1 TAF2_DROME	Q24325 drosophila
17	45	53.6	97	2 Q91ME9	Q91me9 chilli leaf
18	45	53.6	97	2 Q91P83	Q91p83 tomato leaf
19	45	53.6	128	2 Q833V1	Q833v1 enterococcu
20	45	53.6	312	2 Q9N126	Q9n126 bos taurus
21	45	53.6	467	2 Q7YQJ7	Q7yqj7 aus scrofa
22	45	53.6	477	2 Q18150	Q18150 caenorhabdi
23	44	52.4	125	2 Q9NV61	Q9nv61 homo sapien
24	44	52.4	242	2 Q8N6C5	Q8n6c5 homo sapien
25	44	52.4	242	2 Q8BXK6	Q8bxk6 mus musculu
26	44	52.4	287	2 Q8HZ72	Q8hz72 didelphis m
27	44	52.4	287	2 Q8HZ73	Q8hz73 didelphis m
28	44	52.4	377	2 Q92T32	Q92t32 rhizobium m
29	44	52.4	695	2 Q9UZG1	Q9uzg1 pyrococcus
30	44	52.4	777	1 YD81_SCHPO	Q10146 schizosacch
31	44	52.4	1305	1 RRPL_AHSV9	Q70695 african hor

32	44	52.4	1437	2	O15070	O15070 homo sapien
33	43	51.2	78	2	Q7NFI1	Q7nfi1 Gloeobacter
34	43	51.2	205	2	Q82TE1	Q82tel nitrosomona
35	43	51.2	278	2	Q946H8	Q946h8 oryza sativ
36	43	51.2	278	2	Q6ERU5	Q6erus oryza sativ
37	43	51.2	286	2	Q7VZ12	Q7vzi2 bordetella
38	43	51.2	286	2	Q7WSY0	Q7wsy0 bordetella
39	43	51.2	286	2	Q7WGN4	Q7wgn4 bordetella
40	43	51.2	341	1	NAGZ_SALTY	Q8zq16 salmonella
41	43	51.2	341	1	NAGZ_SALTY	Q8zq06 salmonella
42	43	51.2	354	2	Q8VM74	Q8vm74 rhizobium s
43	43	51.2	360	2	Q84GT8	Q84gt8 myxococcus
44	43	51.2	406	2	Q944S7	Q944s7 arabidopsis
45	43	51.2	467	2	Q72C38	Q72c38 desulfovibr

ALIGNMENTS

RESULT 1

Q9TR78 PRELIMINARY; PRT; 17 AA.
AC Q9TR78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-BOTROPIC complex 48,000 SUBUNIT (Fragment).
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE.
RX MEDLINE=95149299; PubMed=7846694; DOI=10.1016/0041-0101(94)90353-0;
RA Perales J., Mousatche H., Marangoni S., Oliveira B., Domont G.B.;
RT "Isolation and partial characterization of an anti-bothropic complex
RL from the serum of South American Didelphidae.";
RL Toxicol 32:1237-1249(1994).
SQ SEQUENCE 17 AA; 1947 MW; CB55FB40E73B2A2A CRC64;

Query Match .100.0%; Score 84; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.le-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWKTE 15

Db 1 LKAMDPTPLWKTE 15

RESULT 2

DM43_DIDMR STANDARD; PRT; 291 AA.
AC P82957;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom metalloproteinase inhibitor DM43.
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Serum;
RA MEDLINE=21955368; PubMed=11815628; DOI=10.1074/jbc.M200589200;
RA Neves-Ferreira A.G.C., Perales J., Fox J.W., Shannon J.D.,
RA Makino D.L., Garratt R.C., Domont G.B.;
RT "Structural and functional analyses of DM43, a snake venom
RT metalloproteinase inhibitor from Didelphis marsupialis serum.";
RL J. Biol. Chem. 277:13129-13137(2002).
CC -I- FUNCTION: Metalloproteinase inhibitor.
CC -I- SUBUNIT: Homodimer.
CC -I- TISSUE SPECIFICITY: Blood and milk.

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CC -!- PTM: N-glycosylated.
CC -!- MASS SPECTROMETRY: MW=42691; METHOD=WALDI; RANGE=1-291;
CC -!- NOTE=Ref.1.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR011015; LEM_like.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Metalloprotease inhibitor; Repeat.
FT DOMAIN 22 79
FT DOMAIN 114 171
FT DOMAIN 191 288
FT DISULFID 28 74
FT DISULFID 121 163
FT DISULFID 213 265
FT CARBOHYD 23 23
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 175 175
FT CARBOHYD 175 175
SQ SEQUENCE 291 AA; 32390 MW; 17A496227E69A65B CRC64;

Query Match 100.0%; Score 84; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDTPPLWKTE 15
DB 1 LKAMDTPPLWKTE 15

RESULT 3
QBHZ75
ID Q8HZ75 PRELIMINARY; PRT; 140 AA.
AC Q8HZ75;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Alpha 1B glycoprotein DVOP51-D (Fragment).
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
RP SEQUENCE FROM N.A.
RA Martinez M.E., Pierce J.R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY131000; AAN06911.1; -.
DR HSSP; O76036; IOLL.
DR InterPro; IPR007110; Ig-like.
FT NON TER 1
FT NON TER 140
SQ SEQUENCE 140 AA; 15297 MW; E19D071A76A5A7F CRC64;

Query Match 89.3%; Score 75; DB 2; Length 140;
Best Local Similarity 93.3%; Pred. No. 0.0007;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDTPPLWKTE 15
DB 42 LKAMDTPPLWKTE 56

RESULT 4
QBHZ74
ID Q8HZ74 PRELIMINARY; PRT; 291 AA.
AC Q8HZ74;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Alpha 1B glycoprotein DVOP114 (Fragment).
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
NCBI_TaxID=9267;
SEQUENCE FROM N.A.
Martinez M.E., Pierce J.R.;
Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AY131000; AAN06911.1; -.
HSSP; O76036; IOLL.
InterPro; IPR007110; Ig-like.
NON TER 1
NON TER 140
SEQUENCE 140 AA; 15297 MW; E19D071A76A5A7F CRC64;

Query Match 89.3%; Score 75; DB 2; Length 140;
Best Local Similarity 93.3%; Pred. No. 0.0007;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDTPPLWKTE 15
DB 42 LKAMDTPPLWKTE 56

RESULT 5
QBHYX5
ID Q8HYX5 PRELIMINARY; PRT; 314 AA.
AC Q8HYX5;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Venom metalloproteinase inhibitor DM43b precursor.
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE FROM N.A.
RA Trugilho M.R.O., Junqueira-de-Azevedo I.L.M., Neves-Ferreira A.G.C.,
RA Domont G.B., Ho P.L., Perales J.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY163806; AAN64698.1; -.
DR HSSP; P24071; IOVZ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW SIGNAL.
FT CHAIN 1 23
FT CHAIN 24 314
SQ SEQUENCE 314 AA; 34604 MW; 69D55F54486D35A5 CRC64;

Query Match 75.0%; Score 63; DB 2; Length 314;
Best Local Similarity 80.0%; Pred. No. 0.12;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDTPPLWKTE 15
DB 24 LKAMDTPPLWKTE 38

RESULT 6
QBMSI3
ID Q8MSI3 PRELIMINARY; PRT; 504 AA.
AC Q8MSI3;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

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DE Venom myotoxin inhibitor DM64 precursor.
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22361219; PubMed=12473101;
RA Rocha S.L., Lomonte B., Neves-Ferreira A.G., Trugilho M.R.,
RA Junqueira-de-Azevedo I.L.M., Ho P.L., Domont G.B., Perales J.;
RA Junqueira-De-Azevedo Id I., Ho P.L., Domont G.B., Gutierrez J.M.,
RA Perales J.;
RT "Functional analysis of DM64, an antimyotoxic protein with
RT immunoglobulin-like structure from Didelphis marsupialis serum.";
RL Eur. J. Biochem. 269:6052-6062 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Rocha S.L.G., Neves-Ferreira A.G.C., Trugilho M.R.O.,
RA Junqueira-de-Azevedo I.L.M., Ho P.L., Domont G.B., Perales J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY078384; AAL82794.1; -
DR HSSP; P24071; 1OVZ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS50835; IG_LIKE; 4.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 504 AA; 55975 MW; 0446529ACBA63B9 CRC64;

Query Match 61.9%; Score 52; DB 2; Length 504;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWKTE 15
| | | | | | | | | |
Db 24 LLAMETTPRLWIETE 38

RESULT 7
Q73ZB2
ID Q73ZB2 PRELIMINARY; PRT; 227 AA.
AC Q73ZB2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MAP1691C;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang Q., Anonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017233; AAS04008.1; -
KW Complete proteome.
SQ SEQUENCE 227 AA; 24027 MW; 952EA4962C0EB199 CRC64;

Query Match 59.5%; Score 50; DB 2; Length 227;
Best Local Similarity 72.7%; Pred. No. 9.5;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLW 11
| | | | |
Db 146 LAALDPRLW 156

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RESULT 8
Q7MTQ9
ID Q7MTQ9 PRELIMINARY; PRT; 344 AA.
AC Q7MTQ9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rhodanese-like domain protein.
GN OrderedLocusNames=PG1887;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601 (2003).
DR EMBL; AE017178; AAG66871.1; -
DR TIGR; PG1887; -
DR GO; GO:0004792; F:thiosulfate sulfurtransferase activity; IEA.
DR GO; GO:0008272; P:sulfate transport; IEA.
DR InterPro; IPR001763; Rhodanese-like.
DR InterPro; IPR001307; Thiosulfatrans.
DR Pfam; PF00581; Rhodanese; 1.
DR PROSITE; PS00380; RHODANESE_1; 1.
DR PROSITE; PS50206; RHODANESE_3; 1.
KW Complete proteome.
SQ SEQUENCE 344 AA; 38572 MW; F3D938CD66BF304 CRC64;

Query Match 57.1%; Score 48; DB 2; Length 344;
Best Local Similarity 46.7%; Pred. No. 30;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWKTE 15
| | | | | | | | | |
Db 199 LSACDPNRPWVESE 213

RESULT 9
Q8FNB0
ID Q8FNB0 PRELIMINARY; PRT; 51 AA.
AC Q8FNB0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=CE2235;
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y8-314;
RX MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens.";
RL Genome Res. 13:1572-1579 (2003).
DR EMBL; AP005221; BAC19045.1; -
KW Complete proteome; Hypothetical protein.

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SQ SEQUENCE 51 AA; 5686 MW; 759F3C5BDCCE414A CRC64;
  Query Match 56.0%; Score 47; DB 2; Length 51;
  Best Local Similarity 50.0%; Pred. No. 5.9;
  Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 AMDPTPLWIKT 14
  :|||:|:|
  21 SLDPTPRVWVET 32

Db

RESULT 10
Y4VJ RHISN STANDARD; PRT; 351 AA.
AC Q53718;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical 39.2 kDa protein y4vJ.
GN ORFNames=y4vJ;
OS Rhizobium sp. (strain NGR234).
OC Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
RN [2]
RP SEQUENCE OF 1-279 FROM N.A.
RX MEDLINE=96389014; PubMed=8796346;
RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RT NGR234 using dye terminators and a thermostable 'sequenase': a
RT beginning.";
RL Genome Res. 6:590-600(1996).
CC -!- SIMILARITY: Belongs to the bacterial luciferase oxidoreductase
CC family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z68203; CA924245.1; -.
DR EMBL; AE000101; AAB91898.1; -.
DR InterPro; IPR002103; Bac luciferase.
DR InterPro; IPR011251; Luciferase like.
DR Pfam; PF00296; Bac luciferase; 1
KW Hypothetical protein; Monooxygenase; Oxidoreductase; Plasmid.
SQ SEQUENCE 351 AA; 39158 MW; 866BDE3B8A40C88D CRC64;

  Query Match 56.0%; Score 47; DB 1; Length 351;
  Best Local Similarity 77.8%; Pred. No. 44;
  Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PTPPLWIKT 14
  :|||:|:|
  167 PTPPIWIAT 175

Db

RESULT 11
Q7Q548
ID Q7Q548 PRELIMINARY; PRT; 370 AA.
AC Q7Q548;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCP7225 (Fragment).
GN Name=agCG51396; ORFNames=ENSANGG00000014288;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: Contains 2 C2 domains.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB0100848; EAA07048.1; -.
DR HSSP; P21707; IKSX.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008021; C:synaptic vesicle; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002149; Alatroxin_recept.
DR InterPro; IPR000008; C2.
DR Pfam; PF00168; C2; 2.
DR PRINTS; PR00360; C2DOMAIN.
DR PROSITE; PS50004; C2_DOMAIN_2; 2.
FT NON TER 1
SQ SEQUENCE 370 AA; 40989 MW; C558FDA3D5CD8D8F CRC64;

  Query Match 54.8%; Score 46; DB 2; Length 370;
  Best Local Similarity 54.5%; Pred. No. 66;
  Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPLW 11
  :|||:|:|
  294 IRALDPTNPW 304

Db

RESULT 12
Q9VQP3
ID Q9VQP3 PRELIMINARY; PRT; 634 AA.
AC Q9VQP3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG3327-PB.
GN Name=E23; ORFNames=CG3327;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnikier S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balwle R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delecher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

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RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodok A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Haddad N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houtson K.F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarly C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhou X., Smith H.O.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacle B.J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RL [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RL [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Mirza S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RL [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AE003580; AAF51122.2;
 DR FlyBase; FBgn0020445; E23.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00005; ABC_tran; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding.
 SQ SEQUENCE 634 AA; 72223 MW; A9D0900DCDB04B01 CRC64;
 Query Match 54.8%; Score 46; DB 2; Length 634;
 Best Local Similarity 57.18; Pred. No. 1.2e+02;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 LKAMDPTPLWIKT 14
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 Db 594 LKAQNSTPLWLNT 607
 RESULT 13
 Q9VQP4
 ID Q9VQP4 PRELIMINARY; PRT; 854 AA.
 AC Q9VQP4
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 22, Last annotation update)
 DE CG3327-PA.
 GN Name=E23; ORFNames=CG3327;
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; *Drosophila*.
 OX NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Frannkovich C., Balswin D.,
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 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foele C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodok A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarly C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle B.J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhou X.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).

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RN  SEQUENCE FROM N.A.
RX  MEDLINE=22426065; PubMed=12537568;
RA  Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA  Patel S., Adams M., Champagne M., Dugan S.P., Frisoe E., Hodgson A.,
RA  George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA  Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA  Svrtak R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA  Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT  "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT  melanogaster euchromatic genome sequence.";
RL  Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN  [3]
RX  SEQUENCE FROM N.A.
RX  MEDLINE=22426070; PubMed=12537573;
RA  Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svrtak R.,
RA  Patel S., Frisoe E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA  Ashburner M., Celniker S.E.;
RT  "The transposable elements of the Drosophila melanogaster euchromatin:
RT  a genomic perspective.";
RL  Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN  [4]
RX  SEQUENCE FROM N.A.
RX  MEDLINE=22426069; PubMed=12537572;
RA  Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA  Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA  Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA  Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA  Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA  Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA  Lewis S.E.;
RT  "Annotation of the Drosophila melanogaster euchromatic genome: a
RT  systematic review.";
RL  Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN  [5]
RX  SEQUENCE FROM N.A.
RG  FlyBase;
RN  Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN  [6]
RX  SEQUENCE FROM N.A.
RG  FlyBase;
RN  Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC  -!- SIMILARITY: Belongs to the ABC transporter family.
DR  EMBL; AE003580; AAF51121.2; -.
DR  IntAct; Q9VQ4; -.
DR  FlyBase; FBgn0020445; E23.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0005524; F:ATP binding; IEA.
DR  GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR  GO; GO:0000166; F:nucleotide binding; IEA.
DR  GO; GO:0006810; P:transport; IEA.
DR  InterPro; IPR003593; AAA_ATPase.
DR  Pfam; PF00005; ABC_tran; 1.
DR  ProDom; PD000006; ABC_transporter; 1.
DR  SMART; SM00382; AAA; 1.
DR  PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR  PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW  ATP-binding.
SQ  SEQUENCE 854 AA; 95085 MW; 721F48827CABD401 CRC64;

Query Match 54.8%; Score 46; DB 2; Length 854;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPLMIKT 14
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RESULT 15
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DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE CG3327-PC.
GN Name=E23; ORFNames=CG3327;
OC Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan X.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* eu-
 RT chromatin: a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -i- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AE003580; AAS64617.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC transporter.
 DR InterPro; IPR011051; RmlC like cupin.
 DR ProDom; PD000006; ABC transporter; 1.
 DR SMART; SM00382; AAA_1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding.
 SQ SEQUENCE 1017 AA; 112351 MW; D3F096E05E6EC76F CRC64;

 Query Match 54.8%; Score 46; DB 2; Length 1017;
 Best Local Similarity 57.1%; Pred.No. 1.9e+02;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

 QY 1 LKAMDPTPLWIKT 14
 Db 977 LKAQNSTPLWLNT 990

 Search completed: May 26, 2005, 18:43:20
 Job time : 117.6 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2005, 18:17:22 ; Search time 129 Seconds
(without alignments)
44.972 Million cell updates/sec

Title: US-10-047-945-2
Perfect score: 84
Sequence: 1 LKAMDPTPLWIKTE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqpl980s:*
2: Geneseqpl990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	15	2	AAW11575
2	84	100.0	15	2	AAW53841
3	84	100.0	15	7	ABB80223
4	69	82.1	12	7	ABB80225
5	65	77.4	11	7	ABB80226
6	54	64.3	10	2	AAW53843
7	54	64.3	10	7	ABB80222
8	50	59.5	9	7	ABB80227
9	47	56.0	303	4	ABG18144
10	47	56.0	531	6	ABR54218
11	46	54.8	267	3	AAW74721
12	46	54.8	267	3	AAW74718
13	46	54.8	729	4	ABB59797
14	46	54.8	1189	2	AAW56496
15	46	54.8	1213	2	AAW06086
16	46	54.8	1213	2	AAW25029
17	46	54.8	1219	4	ABB62618
18	45	53.6	137	7	ADH88053
19	45	53.6	267	3	AAW74720
20	45	53.6	312	6	ABU62528
21	44	52.4	37	4	ABB42105
22	44	52.4	37	4	AAW75798
23	44	52.4	37	4	AAW62985
24	44	52.4	76	3	AAW54516
25	44	52.4	79	3	AAW54515

26	44	52.4	92	3	AAG54605
27	44	52.4	95	3	AAG54604
28	44	52.4	120	4	AAO10737
29	44	52.4	125	4	AAAB93318
30	44	52.4	156	4	ABG22890
31	44	52.4	242	7	ADB90591
32	44	52.4	299	7	ADB90617
33	44	52.4	1336	6	ABR47496
34	44	52.4	1336	8	ADP18673
35	44	52.4	1457	4	AAU32796
36	43	51.2	8	7	ABB80228
37	43	51.2	286	6	ABU23550
38	43	51.2	316	4	ABG23871
39	43	51.2	341	6	ABU47234
40	43	51.2	341	6	ABU45098
41	43	51.2	341	6	ABU47970
42	43	51.2	393	4	AAW79784
43	43	51.2	496	3	AAG27883
44	43	51.2	522	3	AAG27882
45	43	51.2	687	3	AAG27881

ALIGNMENTS

RESULT 1
AAW11575

ID AAW11575 standard; peptide; 15 AA.

XX AC AAW11575;

XX DT 25-MAR-2003 (revised)

XX DT 20-MAR-1997 (first entry)

XX DE N-terminal peptide from lethal toxin neutralising factor.

XX KW Lethal toxin neutralising factor; LTNF; opossum; bee toxin;
scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.

XX OS Didelphis virginiana.

XX PN US5576297-A.

XX PD 19-NOV-1996.

XX PF 22-SEP-1994; 94US-00310340.

XX PR 10-MAY-1993; 93US-00058387.

XX (LIPP/) LIPPS B V.
(LIPP/) LIPPS F W.

XX PI Lipps FW, Lipps BV;

XX DR WPI; 1997-011287/01.

XX PT Treatment of victims of bee or scorpion stings or plant or bacterial
toxins - by admin. of lethal toxin-neutralising factor or its N-terminal
peptide.

XX PS Claim 7; Col 9; 9pp; English.

XX CC The present sequence is from the N-terminus of a 68 kD protein purified
from the serum of the opossum *Didelphis virginiana*. The full-length
protein is a lethal toxin neutralising factor (LTNF). The use of purified
LTNF or of the chemically synthesised 15mer N-terminal peptide for
treating victims of bee stings, scorpion stings and bacterial or plant
toxins is claimed. The patent disclosure does not provide any evidence
for neutralising activity against these various toxins. There is evidence
of significant neutralising activity of the opossum LTNF and the 15mer
peptide against venom from snakes of the families Crotalidae, Elaphidae,
Hydroliidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 15 AA;

Query Match 100.0%; Score 84; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIKTE 15
 |||||
 DB 1 LKAMDPTPLWIKTE 15

RESULT 2

AAW53841

ID AAW53841 standard; peptide; 15 AA.

XX

AC AAW53841;

XX

DT 08-JUL-1998 (first entry)

XX

DE N-terminus of opoosum LTNF.

XX

KW LTNF; lethal toxin neutralising factor; opoosum; envenomation; therapy;

KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;

KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;

KW histamine reaction treatment.

XX

OS Didelphis virginiana.

XX

FN US5744449-A.

XX

PD 28-APR-1998.

XX

PF 03-JUN-1996; 96US-00657163.

XX

PR 10-MAY-1993; 93US-00058387.

XX

PR 22-SEP-1994; 94US-00310340.

XX

PA (LIPP/) LIPPS B V.

XX

PA (LIPP/) LIPPS F W.

XX

PI Lipps FW, Lipps BV;

XX

PS WPI; 1998-271108/24.

XX

DR Lethal Toxin Neutralising Factor peptide from opoosum - can neutralise

XX venom(s) from all major families of poisonous snakes.

XX Claim 1; Col 11; l1pp; English.

XX This sequence represents the peptide of the invention. It is a Lethal

XX Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic

XX protein derived from an opoosum. The peptide can be used in a method for

XX treating a victim of envenomation from a poisonous snake, preferably a

XX poisonous snake from the family of Elapidae, Viperidae or sea snake. It

XX is useful for the treatment of snake bites, sepsis, allergies caused by

XX the environment and treatment of bee or scorpion stings or toxicities

XX caused by plant or bacterial toxins. The peptide can also be used in

XX histamine reaction treatment. The peptide can be used in envenomation

XX treatment for a variety of snakes without prior identification of the

RESULT 3

ABB80223

ID ABB80223 standard; peptide; 15 AA.

XX

AC ABB80223;

XX

DT 06-NOV-2003 (first entry)

XX

DE Synthetic LTNF, LT-15.

XX

Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 Graves' disease; Addison's disease; Hodgkin's disease; depression;
 saliva; ELISA.

XX

OS Synthetic.

XX

FN WO2003060471-A2.

XX

PD 24-JUL-2003.

XX

PF 14-JAN-2003; 2003WO-US001044.

XX

PR 14-JAN-2002; 2002US-00047945.

XX

PA (LIPP/) LIPPS B V.

XX

PA (LIPP/) LIPPS F W.

XX

PI Lipps BV, Lipps FW;

XX

DR WPI; 2003-636703/60.

XX

Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 asthma or diabetes, by employing an ELISA on a saliva sample from a
 patient.

XX

PS Claim 3; Page 3; 24pp; English.

XX

The sequences given in ABB80222-28 represent lethal toxin neutralising
 factor (LTNF) peptides which may be used for reducing elevated levels of
 serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 particular, the methods of the invention are useful for diagnosing and
 treating conditions with elevated serum IGE levels, e.g. asthma,
 diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 Addison's disease or Hodgkin's disease) or depression. The efficacy of
 the protein may be monitored by assaying a human endogenous protein by
 performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 sample using an anti-serum that is specific for the protein. Saliva
 collection is relatively non-invasive when compared to blood collection
 for serum. Saliva can be centrifuged immediately, whereas blood requires
 clotting time before centrifugation to separate serum. Saliva proteins
 can be assayed by a simple ELISA test, whereas an assay of proteins from
 serum requires a more complicated sandwich type ELISA

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 84; DB 7; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIKTE 15

DB 1 LKAMDPTPLWIKTE 15

RESULT 4

ABB80225


```

ID  ABB80225 standard; peptide; 12 AA.
AC  ABB80225;
XX
XX
DT  06-NOV-2003 (first entry)
XX
XX
DE  Synthetic LTNP, LT-12.
XX
XX
KW  Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
KW  IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW  ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KW  SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW  Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW  saliva; ELISA.
XX
XX  Synthetic.
XX
XX  WO2003060471-A2.
XX
XX  24-JUL-2003.
XX
XX  14-JAN-2003; 2003WO-US001044.
XX
XX  14-JAN-2002; 2002US-00047945.
XX
XX  (LIPP/) LIPPS B V.
XX  (LIPP/) LIPPS F W.
XX
XX  Lipps BV, Lipps FW;
XX
XX  WPI; 2003-636703/60.
XX
XX  Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
XX  insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
XX  asthma or diabetes, by employing an ELISA on a saliva sample from a
XX  patient.
XX
XX  Claim 7; Page 4; 24pp; English.
XX
XX  The sequences given in ABB80222-28 represent lethal toxin neutralising
XX  factor (LTNP) peptides which may be used for reducing elevated levels of
XX  serum proteins selected from immunoglobulin E (IgE), nerve growth factor
XX  (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
XX  particular, the methods of the invention are useful for diagnosing and
XX  treating conditions with elevated serum IgE levels, e.g. asthma,
XX  diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
XX  arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
XX  Addison's disease or Hodgkin's disease) or depression. The efficacy of
XX  the protein may be monitored by assaying a human endogenous protein by
XX  performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
XX  sample using an anti-serum that is specific for the protein. Saliva
XX  collection is relatively non-invasive when compared to blood collection
XX  for serum. Saliva can be centrifuged immediately, whereas blood requires
XX  clotting time before centrifugation to separate serum. Saliva proteins
XX  can be assayed by a simple ELISA test, whereas an assay of proteins from
XX  serum requires a more complicated sandwich type ELISA
XX
XX  Sequence 12 AA;
XX
XX  Query Match      82.1%; Score 69; DB 7; Length 12;
XX  Best Local Similarity 100.0%; Pred. No. 0.0004;
XX  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  Qy      1 LKAMDPTPLWI 12
XX          |||||
XX  Db      1 LKAMDPTPLWI 12
XX
XX  RESULT 5
XX  ABB80226
XX  ID  ABB80226 standard; peptide; 11 AA.
XX
XX  AC  ABB80226;
XX
XX
XX
DT  06-NOV-2003 (first entry)
XX
XX
DE  Synthetic LTNP, LT-11.
XX
XX
KW  Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
KW  IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW  ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KW  SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW  Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW  saliva; ELISA.
XX
XX  Synthetic.
XX
XX  WO2003060471-A2.
XX
XX  24-JUL-2003.
XX
XX  14-JAN-2003; 2003WO-US001044.
XX
XX  14-JAN-2002; 2002US-00047945.
XX
XX  (LIPP/) LIPPS B V.
XX  (LIPP/) LIPPS F W.
XX
XX  Lipps BV, Lipps FW;
XX
XX  WPI; 2003-636703/60.
XX
XX  Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
XX  insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
XX  asthma or diabetes, by employing an ELISA on a saliva sample from a
XX  patient.
XX
XX  Claim 7; Page 4; 24pp; English.
XX
XX  The sequences given in ABB80222-28 represent lethal toxin neutralising
XX  factor (LTNP) peptides which may be used for reducing elevated levels of
XX  serum proteins selected from immunoglobulin E (IgE), nerve growth factor
XX  (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
XX  particular, the methods of the invention are useful for diagnosing and
XX  treating conditions with elevated serum IgE levels, e.g. asthma,
XX  diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
XX  arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
XX  Addison's disease or Hodgkin's disease) or depression. The efficacy of
XX  the protein may be monitored by assaying a human endogenous protein by
XX  performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
XX  sample using an anti-serum that is specific for the protein. Saliva
XX  collection is relatively non-invasive when compared to blood collection
XX  for serum. Saliva can be centrifuged immediately, whereas blood requires
XX  clotting time before centrifugation to separate serum. Saliva proteins
XX  can be assayed by a simple ELISA test, whereas an assay of proteins from
XX  serum requires a more complicated sandwich type ELISA
XX
XX  Sequence 11 AA;
XX
XX  Query Match      77.4%; Score 65; DB 7; Length 11;
XX  Best Local Similarity 100.0%; Pred. No. 0.0016;
XX  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  Qy      1 LKAMDPTPLW 11
XX          |||||
XX  Db      1 LKAMDPTPLW 11
XX
XX  RESULT 6
XX  AAW53843
XX  ID  AAW53843 standard; peptide; 10 AA.
XX
XX  AC  AAW53843;
XX
XX  DT  08-JUL-1998 (first entry)
XX
XX

```

```

DE N-terminus of opossum LTNF.
XX
XX LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;
KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
KW histamine reaction treatment.
XX
XX Didelphis virginiana.
OS
XX
XX US5744449-A.
XX
XX 28-APR-1998.
XX
XX 03-JUN-1996; 96US-00657163.
XX
XX 10-MAY-1993; 93US-00058387.
XX
XX 22-SEP-1994; 94US-00310340.
XX
XX (LIPP/) LIPPS B V.
PA
PA (LIPP/) LIPPS F W.
XX
XX Lipps FW, Lipps BV;
XX
XX WPI; 1998-271108/24.
XX
XX Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
PT venom(s) from all major families of poisonous snakes.
XX
XX Claim 7; Col 11; lipp; English.
XX
XX This sequence represents the peptide of the invention. It is a Lethal
CC Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic
CC protein derived from an opossum. The peptide can be used in a method for
CC treating a victim of envenomation from a poisonous snake, preferably a
CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
CC is useful for the treatment of snake bites, sepsis, allergies caused by
CC the environment and treatment of bee or scorpion stings or toxicities
CC caused by plant or bacterial toxins. The peptide can also be used in
CC histamine reaction treatment. The peptide can be used in envenomation
CC treatment for a variety of snakes without prior identification of the
CC snake. Being short it can be synthetically prepared rather than the
CC current production in horses, where some people can show hypersensitivity
CC to horse proteins
XX
XX Sequence 10 AA;
SQ
Query Match 64.3%; Score 54; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTPPL 10
Db 1 LKAMDPTPPL 10
RESULT 7
ABB80222
ID ABB80222 standard; peptide; 10 AA.
XX
XX ABB80222;
XX
XX 06-NOV-2003 (first entry)
XX
XX Synthetic LTNF, LT-10.
XX
XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW saliva; ELISA.
XX
XX Synthetic.
OS

```

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XX
XX WO2003060471-A2.
XX
XX 24-JUL-2003.
XX
XX 14-JAN-2003; 2003WO-US001044.
XX
XX 14-JAN-2002; 2002US-00047945.
XX
XX (LIPP/) LIPPS B V.
PA
PA (LIPP/) LIPPS F W.
XX
XX Lipps BV, Lipps FW;
XX
XX WPI; 2003-636703/60.
XX
XX Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT asthma or diabetes, by employing an ELISA on a saliva sample from a
PT patient.
XX
XX Claim 7; Page 3; 24pp; English.
XX
XX The sequences given in ABB80222-28 represent lethal toxin neutralising
CC factor (LTNF) peptides which may be used for reducing elevated levels of
CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor
CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
CC particular, the methods of the invention are useful for diagnosing and
CC treating conditions with elevated serum IgE levels, e.g. asthma,
CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
CC the protein may be monitored by assaying a human endogenous protein by
CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
CC sample using an anti-serum that is specific for the protein. Saliva
CC collection is relatively non-invasive when compared to blood collection
CC for serum. Saliva can be centrifuged immediately, whereas blood requires
CC clotting time before centrifugation to separate serum. Saliva proteins
CC can be assayed by a simple ELISA test, whereas an assay of proteins from
CC serum requires a more complicated sandwich type ELISA
XX
XX Sequence 10 AA;
SQ
Query Match 64.3%; Score 54; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTPPL 10
Db 1 LKAMDPTPPL 10
RESULT 8
ABB80227
ID ABB80227 standard; peptide; 9 AA.
XX
XX ABB80227;
XX
XX 06-NOV-2003 (first entry)
XX
XX Synthetic LTNF, LT-9.
XX
XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW saliva; ELISA.
XX
XX Synthetic.
OS
XX
XX WO2003060471-A2.
XX

```

PD 24-JUL-2003.
 XX
 PF 14-JAN-2003; 2003WO-US001044.
 XX
 PR 14-JAN-2002; 2002US-00047945.
 XX
 PA (LIPPP/) LIPPS B V.
 PA (LIPPP/) LIPPS F W.
 XX
 PF Lipps BV, Lipps FW;
 XX
 DR WPI; 2003-636703/60.
 XX
 XX Assaying a human endogenous protein (e.g. IgG, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 XX
 PS Claim 7; Page 4; 24pp; English.
 XX
 CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IgE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 XX
 SQ Sequence 9 AA;
 Query Match 59.5%; Score 50; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LKAMDPTPP 9
 |||||
 Db 1 LKAMDPTPP 9
 RESULT 9
 ABG18144
 ID ABG18144 standard; protein; 303 AA.
 XX
 AC ABG18144;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #18135.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 FN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX

(HYSE-) HYSEQ INC.
 Dmanac RT, Liu C, Tang YT;
 WPI; 2001-639362/73.
 N-PSDB; AAS82331.
 New isolated polynucleotide and encoded polypeptides, useful in
 diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits and to assess
 biodiversity.
 Claim 20; SEQ ID NO 48503; 103pp; English.
 The invention relates to isolated polynucleotide (I) and polypeptide (II)
 sequences. (I) is useful as hybridisation probes, polymerase chain
 reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 and in recombinant production of (II). The polynucleotides are also used
 in diagnostics as expressed sequence tags for identifying expressed
 genes. (I) is useful in gene therapy techniques to restore normal
 activity of (II) or to treat disease states involving (II). (II) is
 useful for generating antibodies against it, detecting or quantitating a
 polypeptide in tissue, as molecular weight markers and as a food
 supplement. (II) and its binding partners are useful in medical imaging
 of sites expressing (II). (I) and (II) are useful for treating disorders
 involving aberrant protein expression or biological activity. The
 polypeptide and polynucleotide sequences have applications in
 diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits to assess biodiversity
 and to produce other types of data and products dependent on DNA and
 amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 amino acid sequences of the invention. Note: The sequence data for this
 patent did not appear in the printed specification, but was obtained in
 electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences
 Sequence 303 AA;
 Query Match 56.0%; Score 47; DB 4; Length 303;
 Best Local Similarity 42.9%; Pred. No. 35;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 KAMDPTPLWKTE 15
 :|||:::
 Db 39 EASDPVPVWRLQ 52
 RESULT 10
 ABR54218
 ID ABR54218 standard; protein; 531 AA.
 XX
 AC ABR54218;
 XX
 DT 23-JUN-2003 (first entry)
 XX
 DE Human NOV21a protein SEQ ID NO:104.
 XX
 KW Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
 KW anorectic; immunosuppressive; cytostatic; antidiabetic; antifertility;
 KW haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator;
 KW neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaeamic;
 KW gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma;
 KW congenital heart defect; aortic stenosis; valve disease; transplantation;
 KW tuberosus sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
 KW prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;
 KW fertility; haemophilia; hypercoagulation; graft versus host disease;
 KW idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
 KW Crohn's disease; multiple sclerosis; infectious disease; cancer;
 KW cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia;
 XX
 OS Homo sapiens.

[illegible]

```

CC used in gene therapy protocols
XX SQ Sequence 267 AA;
    Query Match      54.8%; Score 46; DB 3; Length 267;
    Best Local Similarity 58.3%; Pred. No. 45;
    Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 3 AMDPTPLWIKT 14
Db 9 AKHPTPTWLQT 20
    |||||:::
    |||||:::

RESULT 12
AAY74718
ID AAY74718 standard; protein; 267 AA.
XX
XX
AC AAY74718;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 241 protein sequence SEQ ID NO:910.
XX
DE Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy.
XX
XX Neisseria meningitidis.
OS
XX WO9957280-A2.
PN
XX PD 11-NOV-1999.
XX
XX PF 30-APR-1999; 99WO-US009346.
XX
PR 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
XX (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
XX Fraser C, Galeotti C, Grandi G, Hickey E, Massignani V, Mora M;
PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
XX WPI; 2000-062150/05.
DR N-PSDB; AAZ53480.
XX
XX Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
XX Claim 2; Page 553; 1453pp; English.
XX
XX AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols
XX

SQ Sequence 267 AA;
    Query Match      54.8%; Score 46; DB 3; Length 267;
    Best Local Similarity 58.3%; Pred. No. 45;
    Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 3 AMDPTPLWIKT 14
Db 9 AKHPTPTWLQT 20
    |||||:::
    |||||:::

RESULT 13
ABB59797
ID ABB59797 standard; protein; 729 AA.
XX
XX
AC ABB59797;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 6183.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
XX WO200171042-A2.
PN
XX PD 27-SEP-2001.
XX
XX PF 23-MAR-2001; 2001WO-US009231.
XX
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE ) PE CORP NY.
PA
XX Venter JC, Adams M, Li FWD, Myers EW;
PI WPI; 2001-656860/75.
XX N-PSDB; ABL03900.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
XX Disclosure; SEQ ID NO 6183; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_sequences
XX
XX SQ Sequence 729 AA;
    Query Match      54.8%; Score 46; DB 4; Length 729;
    Best Local Similarity 57.1%; Pred. No. 1.3e+02;
    Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 1 LKAMDPTPLWIKT 14
Db 689 LKQNSTSPWLNT 702
    |||||:::
    |||||:::

RESULT 14
AAR56496
ID AAR56496 standard; protein; 1189 AA.

```

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XX AAR56496;
AC
XX
XX 25-MAR-2003 (revised)
DT 23-MAR-1995 (first entry)
XX
XX TATA-binding protein-associated factor dTAFI50.
DE
XX TATA-binding protein associated factor; dTAFI50; screening; diagnostic;
KW therapeutic; gene transcription regulation.
XX
XX Drosophila.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 923
FT /note= "Val or Leu"
FT Misc-difference 1106
FT /note= "Arg, Pro or His"
FT Misc-difference 1172
FT /note= "STOP"
FT Misc-difference 1176
FT /note= "STOP"
XX
XX WO9417087-A1.
PN
XX
XX 04-AUG-1994.
PD
XX
XX 28-JAN-1994; 94WO-US001114.
PF
XX
XX 28-JAN-1993; 93US-00013412.
PR 30-JUN-1993; 93US-00087119.
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX
XX Tjian R, Comai L, Dynlacht BD, Hoey T, Ruppert S, Tanese N;
PI Wang E, Weinzierl ROJ;
XX
XX WPI; 1994-264019/32.
DR N-PSDB; AAQ70733.
XX
XX TATA-binding protein associated protein factors - and corresponding
FT nucleotide sequence and deriv. antibodies, useful in screening,
PT diagnostics and therapeutics.
XX
XX Disclosure; Page 156; 180pp; English.
PS
XX
XX The TATA-binding protein associated factor hTAFI50 (including specific
CC antibodies and fusion products) are used in drug screening, diagnostics
CC and therapeutics. They are used in the development of specific
CC biochemical assays for screening compounds that agonise or antagonise
CC selected transcription factors involved in regulating gene expression
CC associated with human pathology. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 1189 AA;
SQ
Query Match 54.8%; Score 46; DB 2; Length 1189;
Best Local Similarity 53.3%; Pred. No. 2.1e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPPLWIKTE 15
| | | | | | | | | | | | | | | |
Db 589 LSAMDDSPVLWIRLD 603

RESULT 15
AAW06086
ID AAW06086 standard; protein; 1213 AA.
XX
XX AAW06086;
AC
XX
XX 25-MAR-2003 (revised)
DT 27-JAN-1997 (first entry)

```

```

XX Drosophila TATA-binding protein associated factor dTAFI1150 protein.
DE
XX
XX Drosophila; TATA-binding protein; TBP associated factor; TFIID;
KW RNA polymerase II; transcription; messenger RNA; nuclear fraction;
KW holoenzyme; lambda-gt11; expression library.
XX
XX Drosophila melanogaaster.
OS
XX US5534410-A.
PN
XX
XX 09-JUL-1996.
PD
XX
XX 28-JAN-1994; 94US-00188582.
PF
XX
XX 28-JAN-1993; 93US-00013412.
PR 30-JUN-1993; 93US-00087119.
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX
XX Comai L, Hoey T, Tanese N, Ruppert S, Weinzierl ROJ, Tjian R;
PI Wang E, Dynlacht BD;
XX
XX WPI; 1996-333245/33.
DR N-PSDB; AAT42219.
XX
XX Screen for cpds. that bind human TATA-binding protein associated factor -
FT by testing ability to bind to polypeptide fragments of the factor, useful
PT as (ant)agonists of transcription factors involved in disease.
XX
XX Example; Col 123-132; 86pp; English.
XX
XX This is the amino acid sequence of the Drosophila TATA-binding protein
CC (TBP) associated factor (TAF) designated TAFI160. The protein is a
CC component of the TFIID fraction required for reconstituting RNA
CC polymerase II in vitro transcription activity. The encoded protein has an
CC estimated mol. wt. of 60 kD by SDS-PAGE. The invention relates to
CC purified proteins involved in transcription by RNA polymerase II, the RNA
CC polymerase which transcribes messenger RNA. RNA polymerase II
CC transcription proceeds in vitro upon addition of several nuclear
CC fractions designated TFIIA, B, D, E, F, H, I and J to RNA polymerase II
CC holoenzyme. Fraction TFIID has been shown to contain a TBP and other
CC TAFs. Purification of TFIID and separation of its components reveals 7
CC proteins ranging in size from 30-250 kD. Serum raised against the TFIID
CC fraction allowed cloning of the corresp. genes from lambda-gt11
CC expression libraries. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 1213 AA;
SQ
Query Match 54.8%; Score 46; DB 2; Length 1213;
Best Local Similarity 53.3%; Pred. No. 2.2e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPPLWIKTE 15
| | | | | | | | | | | | | | | |
Db 620 LSAMDDSPVLWIRLD 634

Search completed: May 26, 2005, 18:36:52
Job time : 133 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:43:39 ; Search time 98.4 Seconds
(without alignments)
52.587 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKAMDPTPLWKITE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	15	14	US-10-047-945-2
2	69	82.1	12	14	US-10-047-945-4
3	65	77.4	11	14	US-10-047-945-5
4	54	64.3	10	14	US-10-047-945-1
5	50	59.5	9	14	US-10-047-945-6
6	47	56.0	531	15	US-10-236-417-104
7	46	54.8	85	15	US-10-424-599-278038
8	46	54.8	384	16	US-10-437-963-200494
9	45	53.6	41	15	US-10-424-599-173148
10	45	53.6	312	10	US-09-885-303A-16
11	44	52.4	37	9	US-09-864-761-45321
12	44	52.4	70	15	US-10-424-599-229035
13	44	52.4	106	15	US-10-424-599-255201

14	44	52.4	124	15	US-10-424-599-151167	Sequence 151167,
15	44	52.4	144	15	US-10-424-599-205702	Sequence 205702,
16	44	52.4	158	15	US-10-425-114-63058	Sequence 63058, A
17	44	52.4	530	15	US-10-424-599-283741	Sequence 283741,
18	44	52.4	1336	14	US-10-177-293-228	Sequence 228, App
19	43	51.2	8	14	US-10-047-945-7	Sequence 7, Appli
20	43	51.2	129	16	US-10-437-963-168841	Sequence 168841,
21	43	51.2	156	16	US-10-437-963-114167	Sequence 114167,
22	43	51.2	258	16	US-10-437-963-197262	Sequence 197262,
23	43	51.2	278	16	US-10-437-963-197265	Sequence 197265,
24	43	51.2	286	15	US-10-282-122A-51474	Sequence 51474, A
25	43	51.2	341	15	US-10-282-122A-73022	Sequence 73022, A
26	43	51.2	341	15	US-10-282-122A-75158	Sequence 75158, A
27	43	51.2	341	15	US-10-282-122A-75894	Sequence 75894, A
28	43	51.2	840	16	US-10-437-963-144200	Sequence 144200,
29	43	51.2	932	15	US-10-041-018-220	Sequence 220, App
30	42	50.0	82	16	US-10-437-963-128480	Sequence 128480,
31	42	50.0	91	15	US-10-424-599-264272	Sequence 264272,
32	42	50.0	136	16	US-10-767-701-54623	Sequence 54623, A
33	42	50.0	157	16	US-10-767-701-43303	Sequence 43303, A
34	42	50.0	180	16	US-10-437-963-186583	Sequence 186583,
35	42	50.0	370	16	US-10-437-963-188412	Sequence 188412,
36	42	50.0	661	9	US-09-939-825-17	Sequence 17, Appl
37	42	50.0	661	16	US-10-437-963-180606	Sequence 180606,
38	42	50.0	679	9	US-09-764-853-607	Sequence 607, App
39	42	50.0	679	11	US-09-764-875-824	Sequence 824, App
40	42	50.0	728	16	US-10-437-963-133075	Sequence 133075,
41	42	50.0	842	15	US-10-276-774-1735	Sequence 1735, App
42	42	50.0	853	14	US-10-060-036-161	Sequence 161, App
43	42	50.0	910	14	US-10-028-072-112	Sequence 112, App
44	42	50.0	910	14	US-10-140-808-112	Sequence 112, App
45	42	50.0	910	14	US-10-121-049-112	Sequence 112, App

ALIGNMENTS

RESULT 1
US-10-047-945-2
; Sequence 2, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IGB)IMPLICATED DISORDERS
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-2

Query Match 100.0%; Score 84; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWKITE 15

Db 1 LKAMDPTPLWKITE 15

RESULT 2
US-10-047-945-4
; Sequence 4, Application US/10047945
; Publication No. US20030157555A1

; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.
US-10-047-945-4

Query Match 82.1%; Score 69; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWI 12
| | | | | | | | | | | | | |
Db 1 LKAMDPTPLWI 12

RESULT 3
US-10-047-945-5
; Sequence 5, Application US/10047945
; Publication No. US20030157555A1

; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.
US-10-047-945-5

Query Match 77.4%; Score 65; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLW 11
| | | | | | | | | | | |
Db 1 LKAMDPTPLW 11

RESULT 4
US-10-047-945-1
; Sequence 1, Application US/10047945

; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-1

Query Match 64.3%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPL 10
| | | | | | | | | |
Db 1 LKAMDPTPL 10

RESULT 5
US-10-047-945-6
; Sequence 6, Application US/10047945
; Publication No. US20030157555A1

; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.
US-10-047-945-6

Query Match 59.5%; Score 50; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPP 9
| | | | | | | | |
Db 1 LKAMDPTPP 9

RESULT 6
US-10-236-417-104
; Sequence 104, Application US/10236417
; Publication No. US20040048256A1
; GENERAL INFORMATION:


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; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442C
; CURRENT APPLICATION NUMBER: US/10/236.417
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US60/318.120
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: US60/318.430
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US60/322.781
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/318.184
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/361.663
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US60/396.412
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US60/322.636
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322.817
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322.816
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/323.519
; PRIOR FILING DATE: 2001-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 104
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-417-104

Query Match      56.0%; Score 47; DB 15; Length 531;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy
Db      70 MDTSPPLWLTLE 81

RESULT 7
US-10-424-599-278038
; Sequence 278038, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424.599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278038
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93091C.1.pep
US-10-424-599-278038

Query Match      54.8%; Score 46; DB 15; Length 85;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy
Db      45 TPPLWVWIKIE 53

US-10-047-945-2.open.rapb
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RESULT 8
US-10-437-963-200494
; Sequence 200494, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437.963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 200494
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95958C.1.pep
US-10-437-963-200494

Query Match      54.8%; Score 46; DB 16; Length 384;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AMDPTPLWIKT 14
Db      91 AAAPAPPLWLT 102

RESULT 9
US-10-424-599-173148
; Sequence 173148, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424.599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 173148
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_127369C.1.pep
US-10-424-599-173148

Query Match      53.6%; Score 45; DB 15; Length 41;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      5 DPTPLWIKTE 15
Db      14 DPPLWVWQPE 24

RESULT 10
US-09-885-303A-16
; Sequence 16, Application US/09885303A
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; Publication No. US20030032078A1
; GENERAL INFORMATION:
; APPLICANT: TRAVIS, GABRIEL H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF MACULAR
; DEGENERATION AND RETINAL DEGENERATIONS
; FILE REFERENCE: UTSD:758US
; CURRENT APPLICATION NUMBER: US/09/885,303A
; PRIOR APPLICATION NUMBER: 60/263,837
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 16
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Bos taurus
; US-09-885-303A-16

Query Match          53.6%; Score 45; DB 10; Length 312;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIKT 14
   |||||:|:::|
Db 268 LKAMDPSGLYVRT 281

RESULT 11
US-09-864-761-45321
; Sequence 45321, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
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; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45321
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL133458.11
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68
; OTHER INFORMATION: SWISSPROT HIT: O53951, EVALUE 6.40e-00
; OTHER INFORMATION: EST_HUMAN HIT: AI986481.1, EVALUE 6.00e-16
; US-09-864-761-45321

Query Match          52.4%; Score 44; DB 9; Length 37;
Best Local Similarity 46.2%; Pred. No. 22;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPLWIKT 14
   |||||:|:::|
Db 5 KSMGPAPPRWRS 17

RESULT 12
US-10-424-599-229035
; Sequence 229035, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 229035
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_48845C.1.psp
; US-10-424-599-229035

Query Match          52.4%; Score 44; DB 15; Length 70;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIKTE 15
   |||||:|:::|
Db 55 LKADQKQKFWIKTE 69

RESULT 13
US-10-424-599-255201
; Sequence 255201, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 255201
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_72469C.1.pep
; US-10-424-599-255201

Query Match      52.4%; Score 44; DB 15; Length 106;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      6 PTPPLWI 12
Db      92 PTPPLWV 98
      |||||:

RESULT 14
US-10-424-599-151167
; Sequence 151167, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 151167
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_107527C.1.pep
; US-10-424-599-151167

Query Match      52.4%; Score 44; DB 15; Length 124;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      5 DPTPPLWI 12
Db      96 DPIPPLWV 103
      |||||:

RESULT 15
US-10-424-599-205702
; Sequence 205702, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 205702
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(144)
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; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_27777C.1.pep
; US-10-424-599-205702

Query Match      52.4%; Score 44; DB 15; Length 144;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      6 PTPPLWI 12
Db      28 PTPPLWV 34
      |||||:

Search completed: May 26, 2005, 19:17:13
Job time : 138.4 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:29:58 ; Search time 34.2 Seconds
(without alignments)
32.741 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKAWDPTPLWKTE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	15	1	US-08-310-340A-1
2	84	100.0	15	1	US-08-657-163A-1
3	54	64.3	10	1	US-08-657-163A-2
4	46	54.8	1213	1	US-08-188-582-20
5	46	54.8	1213	1	US-08-646-715-20
6	45	53.6	137	4	US-09-134-000C-5938
7	43	51.2	397	4	US-09-902-540-13316
8	41	48.8	151	4	US-09-732-210-1367
9	41	48.8	4928	3	US-09-270-767-43223
10	41	48.8	4928	3	US-09-036-987A-5
11	41	48.8	4928	3	US-09-370-700-5
12	41	48.8	4928	3	US-09-603-207-5
13	40	47.6	151	4	US-09-732-210-1353
14	40	47.6	198	4	US-09-270-767-57545
15	40	47.6	303	4	US-09-270-767-42501
16	40	47.6	356	4	US-09-270-767-44479
17	40	47.6	360	4	US-09-270-767-42265
18	39.5	47.0	607	2	US-08-878-989-15
19	39.5	47.0	607	3	US-09-272-796-15
20	39	46.4	72	4	US-09-949-016-8760
21	39	46.4	98	2	US-09-047-125-15
22	39	46.4	98	3	US-07-736-335E-15
23	39	46.4	189	4	US-09-710-279-1998
24	39	46.4	206	2	US-08-477-396A-18
25	39	46.4	210	4	US-09-270-767-45215
26	39	46.4	228	4	US-09-710-279-1166
27	39	46.4	285	4	US-09-248-796A-20923

28	39	46.4	286	3	US-09-134-001C-4103	Sequence 4103, Ap
29	39	46.4	382	4	US-09-266-965-104	Sequence 104, Ap
30	39	46.4	412	2	US-08-463-081B-14	Sequence 14, Appl
31	39	46.4	412	2	US-08-461-379A-14	Sequence 14, Appl
32	39	46.4	412	2	US-08-462-390B-14	Sequence 14, Appl
33	39	46.4	412	3	US-08-463-074B-14	Sequence 14, Appl
34	39	46.4	412	3	US-08-465-585C-14	Sequence 14, Appl
35	39	46.4	412	3	US-08-462-624-2	Sequence 2, Appl
36	39	46.4	412	4	US-09-949-016-7219	Sequence 6404, Ap
37	39	46.4	412	4	US-09-949-016-7219	Sequence 7219, Ap
38	38	45.2	87	4	US-09-270-767-41296	Sequence 41296, A
39	38	45.2	87	4	US-09-270-767-56512	Sequence 56512, A
40	38	45.2	168	4	US-09-252-991A-21932	Sequence 21932, A
41	38	45.2	190	4	US-09-328-352-6054	Sequence 21938, A
42	38	45.2	207	4	US-07-857-224B-42	Sequence 6054, Ap
43	38	45.2	267	2	US-09-902-540-14895	Sequence 42, Appl
44	38	45.2	446	4		Sequence 14895, A
45	38	45.2	446	4		

ALIGNMENTS

RESULT 1

US-08-310-340A-1

; Sequence 1, Application US/08310340A

; Patent No. 5576297

; GENERAL INFORMATION:

; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS

; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND

; TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: BINIE V. LIPPS

; STREET: 4509 MIMOSA DR.

; CITY: BELLAIRE

; STATE: TEXAS

; COUNTRY: USA

; ZIP: 77401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB

; COMPUTER: IBM COMPATIBLE

; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1

; SOFTWARE: MS WORD 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/310,340A

; FILING DATE: 22 SEPTEMBER 1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/058, 387

; FILING DATE: 10 MAY 1993

; ATTORNEY/AGENT INFORMATION:

; NAME:

; REGISTRATION NUMBER:

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 713-723-6845

; TELEFAX: 713-663-7290

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15

; TYPE: AMINO ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N

; ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:

; ORGANISM: DIDELPHIS VIRGINIANA

; STRAIN: WILD

INDIVIDUAL ISOLATE: TEXAS WILD
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
VOLUME: SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
US-08-310-340A-1

Query Match 100.0%; Score 84; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDTPPLWKTE 15
DB 1 LKAMDTPPLWKTE 15

RESULT 2

US-08-657-163A-1
Sequence 1, Application US/08657163A
Patent No. 5744449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LTNFS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
TELEX:
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA
STRAIN: WILD
INDIVIDUAL ISOLATE: TEXAS WILD
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
US-08-657-163A-1

Query Match 100.0%; Score 84; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDTPPLWKTE 15
DB 1 LKAMDTPPLWKTE 15

RESULT 3

US-08-657-163A-2
Sequence 2, Application US/08657163A
Patent No. 5744449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LTNFS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514

APPLICATION NUMBER: 08/058.387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: SYNTHETIC
US-08-657-163A-2

Query Match 64.3%; Score 54; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LKAMDPTPL 10
Db 1 LKAMDPTPL 10

RESULT 4
US-08-188-582-20
Sequence 20, Application US/08188582
Patent No. 5534410
GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 28-JAN-1994
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 1213 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-582-20

Query Match 54.8%; Score 46; DB 1; Length 1213;
Best Local Similarity 53.3%; Pred. No. 74;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 LKAMDPTPLWKTE 15
Db 620 LSAMDDSPVLWRLD 634

RESULT 5
US-08-646-715-20
Sequence 20, Application US/08646715
Patent No. 5637686
GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 09-MAY-1996
APPLICATION NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1213 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-715-20

Query Match 54.8%; Score 46; DB 1; Length 1213;
Best Local Similarity 53.3%; Pred. No. 74;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 LKAMDPTPLWKTE 15
Db 620 LSAMDDSPVLWRLD 634

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Db      620 LSAMDDSPVLWIRLD 634

RESULT 6
US-09-134-000C-5938
; Sequence 5938, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5938
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5938

Query Match      53.6%; Score 45; DB 4; Length 137;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 DTPPLWI 12
      :|||||:
Db      85 NPTPLWV 92

RESULT 7
US-09-902-540-13316
; Sequence 13316, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13316
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13316

Query Match      51.2%; Score 43; DB 4; Length 397;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 MDPTPLWI 12
      :|||||:
Db      369 MDPEPRWV 377

RESULT 8
US-09-732-210-1367
; Sequence 1367, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.

; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1367
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Zea mays
US-09-732-210-1367

Query Match      48.8%; Score 41; DB 4; Length 151;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      7 TPPLWIKT 14
      :|||||:
Db      21 TPPTWLKT 28

RESULT 9
US-09-270-767-43223
; Sequence 43223, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43223
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43223

Query Match      48.8%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 MDPTPPL 10
      :|||||:
Db      43 MDPTPPL 49

RESULT 10
US-09-036-987A-5
; Sequence 5, Application US/09036987A
; Patent No. 6143526
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Merlo, Donald J.
; APPLICANT: Turney, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; TITLE OF INVENTION: Production
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow AgroSciences LLC Patent Department
; STREET: 9330 Zionsville Road
```


CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,987A
FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,608
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEFAX: (317)337-4847
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4928 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-036-987A-5

Query Match 48.8%; Score 41; DB 3; Length 4928;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWIKT 14
|:|:|:|:|:
Db 2850 LRAADVSAFLWLAT 2863

RESULT 11

US-09-370-700-5
; Sequence 5, Application US/09370700
; Patent No. 6274350
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J
; APPLICANT: Turner, Jan R
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/370,700
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/36987
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4928
; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-5

Query Match 48.8%; Score 41; DB 3; Length 4928;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWIKT 14
|:|:|:|:|:
Db 2850 LRAADVSAFLWLAT 2863

RESULT 12

US-09-603-207-5
; Sequence 5, Application US/09603207B
; Patent No. 6521406
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J
; APPLICANT: Turner, Jan R
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/603,207B
; CURRENT FILING DATE: 2000-06-23
; EARLIER APPLICATION NUMBER: 09/370,700
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4928
; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-09-603-207-5

Query Match 48.8%; Score 41; DB 4; Length 4928;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWIKT 14
|:|:|:|:|:
Db 2850 LRAADVSAFLWLAT 2863

RESULT 13

US-09-732-210-1353
; Sequence 1353, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1353
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Agaricus bisporus
US-09-732-210-1353

Query Match 47.6%; Score 40; DB 4; Length 151;
Best Local Similarity 75.0%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TPPLWIKT 14
|:|:|:|:|:
Db 21 TPPSWLKT 28

RESULT 14

US-09-767-57545
; Sequence 57545, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57545
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57545

Query Match 47.6%; Score 40; DB 4; Length 198;
Best Local Similarity 54.5%; Pred. No. 95;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPLW 11
Db :||: ||: ||
70 IKAVSPENLW 80

RESULT 15
US-09-270-767-42501
; Sequence 42501, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42501
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-42501

Query Match 47.6%; Score 40; DB 4; Length 303;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 MDPTPLMIKT 14
Db :||: ||: ||
95 LQTPPLWTQT 105

Search completed: May 26, 2005, 19:08:38
Job time : 35.4 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2005, 18:26:23 ; Search time 7.9 Seconds
(without alignments)
60.897 Million cell updates/sec

Title: US-10-047-945-3

Perfect score: 24

Sequence: 1 LKAMD 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	98	2 A11916	hypothetical prote
2	24	100.0	144	2 B83114	50S ribosomal prote
3	24	100.0	145	2 D83424	hypothetical prote
4	24	100.0	178	2 A38593	transcription fact
5	24	100.0	185	1 LZWSG	lysozyme (EC 3.2.1
6	24	100.0	202	2 AE3377	queuine tRNA-ribos
7	24	100.0	210	2 T14734	N85 protein - sorg
8	24	100.0	213	2 F69838	opine aminotransfe
9	24	100.0	237	2 A42013	alpha-1-B-glycopro
10	24	100.0	253	2 JC5709	maleate isomerase
11	24	100.0	256	2 C71546	probable glucosyl-6
12	24	100.0	270	1 CCECID	cell division inhi
13	24	100.0	270	2 AH0724	septum site determ
14	24	100.0	270	2 F85695	cell division inhi
15	24	100.0	270	2 E90837	cell division inhi
16	24	100.0	272	2 E95144	Cof family protein
17	24	100.0	272	2 C98012	conserved hypothet
18	24	100.0	279	2 S58402	synaptotagmin V -
19	24	100.0	304	2 I39049	alpha (1,3) fucosyl
20	24	100.0	305	2 T09370	shikimate kinase h
21	24	100.0	306	2 B54717	palmitoyl-protein
22	24	100.0	359	2 A45156	alpha-(1,3)-fucosyl
23	24	100.0	364	2 I39048	alpha (1,3) fucosyl
24	24	100.0	364	2 S43117	transposase - lept
25	24	100.0	374	2 H87450	conserved hypothet
26	24	100.0	377	2 AD3363	queuine tRNA-ribos
27	24	100.0	379	1 DWDXB	2-hydroxyglutaryl-
28	24	100.0	381	2 B69722	queuine tRNA-ribos
29	24	100.0	385	2 AD0528	conserved hypothet

30 24 100.0 385 2 F90649
31 24 100.0 388 2 F75047
32 24 100.0 389 2 E71113
33 24 100.0 391 2 F85500
34 24 100.0 403 2 S58400
35 24 100.0 412 2 D69525
36 24 100.0 424 2 F81552
37 24 100.0 425 2 S34449
38 24 100.0 428 2 C86504
39 24 100.0 428 2 B72118
40 24 100.0 437 1 A31752
41 24 100.0 437 2 S42111
42 24 100.0 442 2 C69785
43 24 100.0 449 2 G64349
44 24 100.0 461 2 D97243
45 24 100.0 464 2 T17332

ALIGNMENTS

RESULT 1

A11916

hypothetical protein asl0884 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: A11916

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: A11916

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-98 <KUR>

A;Cross-references: UNIPROT:Q8YVG6; GB:BA000019; PIDN:BA000019; PID:gi17130229; GSPDB:G

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: asl0884

C;Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology

Query Match 100.0%; Score 24; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
Db 23 LKAMD 27

RESULT 2

B83114

50S ribosomal protein L15 PA4244 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C;Accession: B83114

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A;Reference number: AB2950; MUID:20437337; PMID:10984043

A;Accession: B83114

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-144 <STO>

A;Cross-references: UNIPROT:Q8HWF4; GB:AE004841; GB:AE004091; NID:G9950451; PIDN:AAG0763

A;Experimental source: strain PA01

C;Genetics:

A;Gene: rplO; PA4244

C;Superfamily: Escherichia coli ribosomal protein L15

Query Match 100.0%; Score 24; DB 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
 |||||
 Db 69 LKAMD 73

RESULT 3
 D83424
 hypothetical protein PA1761 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: D83424
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: D83424
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-145 <STO>
 A:Cross-references: UNIPROT:Q912X8; GB:AE004602; GB:AE004602; NID:g9947739; PIDN:AAG0515
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA1761

Query Match 100.0%; Score 24; DB 2; Length 145;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
 |||||
 Db 22 LKAMD 26

RESULT 4
 A38593
 transcription factor AP-2 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 20-Sep-1999
 C:Accession: A38593; S19218
 R:Mitchell, P.J.; Timmons, P.M.; Hebert, J.M.; Rigby, P.W.J.; Tjian, R.
 Genes Dev. 5, 105-119, 1991
 A>Title: Transcription factor AP-2 is expressed in neural crest cell lineages during mou
 A:Reference number: A38593; MUID:91115091; PMID:1989904
 A:Accession: A38593
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-178 <MIT>
 A:Cross-references: GB:X57012; NID:g50001; PIDN:CAA40331.1; PID:g50002
 C:Superfamily: transcription factor AP-2
 C:Keywords: DNA binding; transcription regulation

Query Match 100.0%; Score 24; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
 |||||
 Db 147 LKAMD 151

RESULT 5
 L2WSG
 lysozyme (EC 3.2.1.17) g [validated] - black swan
 N:Alternate names: 1,4-beta-N-acetylmuramidase; peptidoglycan N-acetylmuramoylhydrolase
 C:Species: Cygnus atratus (black swan)
 C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004

C:Accession: A00872; B34047
 R:Simpson, R.J.; Begg, G.S.; Dorow, D.S.; Morgan, F.J.
 Biochemistry 19, 1814-1819, 1980
 A>Title: Complete amino acid sequence of the goose-type lysozyme from the egg white of t
 A:Reference number: A00872; MUID:80198318; PMID:7378374
 A:Accession: A00872
 A:Molecule type: protein
 A:Residues: 1-185 <SIM>
 A:Cross-references: UNIPROT:P00717
 R:Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
 Biochem. Biophys. Res. Commun. 166, 139-145, 1990
 A>Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
 A:Reference number: A30157; MUID:90147691; PMID:2302197
 A:Accession: B34047
 A:Molecule type: protein
 A:Residues: 'X', 47-59, 'X', 61-68; 95-99, 'X', 101-106, 'X', 110-111 <JA2>
 C:Function:
 A>Description: catalyzes hydrolysis of the beta-1,4-glycosidic bond between N-acetylmura
 C:Superfamily: lysozyme g
 C:Keywords: bacteriolytic enzyme; egg white; glycosidase; hydrolase; polysaccharide degr
 F:4-60.18-29/Disulfide bonds: #status predicted
 F:73.86/Active site: Glu, Asp #status predicted

Query Match 100.0%; Score 24; DB 1; Length 185;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
 |||||
 Db 42 LKAMD 46

RESULT 6
 A83377
 queuine tRNA-ribosyltransferase (EC 2.4.2.29) [imported] - Brucella melitensis (strain 1
 C:Species: Brucella melitensis
 C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: A83377
 R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Loeb, T.; Ivanova,
 ; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
 A:Reference number: AD3252; PMID:11756688
 A:Accession: A83377
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-202 <KUR>
 A:Cross-references: UNIPROT:Q8YH02; GB:AE008917; PIDN:AAL52184.1; PID:g17982964; GSPDB:C
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BME11003
 A:Map position: 1
 C:Keywords: glycosyltransferase; pentosyltransferase

Query Match 100.0%; Score 24; DB 2; Length 202;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
 |||||
 Db 31 LKAMD 35

RESULT 7
 T14734
 NS5 protein - sorghum (fragment)
 C:Species: Sorghum bicolor (sorghum)
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T14734
 R:Sanan, N.; Akam, A.; Bhattacharya, A.; Sopory, S.K.
 submitted to the ENBL Data Library, December 1996
 A:Reference number: Z18176
 A:Accession: T14734

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-210 <SAN>
A;Cross-references: UNIPROT:P93525; EMBL:Y09874; NID:e1012757
A;Experimental source: variety Tx430; leaf

Query Match 100.0%; Score 24; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
|||||
Db 28 LKAMD 32

RESULT 8
F69838
opine aminotransferase homolog yisW - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69838
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteaux, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choudhury, S.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallego, M.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Maueel, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M.; Ogawa, K.; Ogilward, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron, A.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yoshikawa, H.; Yanchin, A.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Yanchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69838
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-213 <KUN>
A;Cross-references: UNIPROT:O06732; GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12928.
A;Experimental source: strain 168
C;Genetics:
A;Gene: yisW

Query Match 100.0%; Score 24; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
|||||
Db 39 LKAMD 43

RESULT 9
A42013
alpha-1-B-glycoprotein - North American opossum (fragments)
C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C;Accession: A42013
R;Cataneese, J.J.; Kress, L.F.
Biochemistry 31, 410-418, 1992
A;Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to human
A;Reference number: A42013; MUID:92118834; PMID:1731898
A;Accession: A42013
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-237 <CAT>
A;Cross-references: UNIPROT:Q28359; GB:J05356
C;Keywords: glycoprotein

Query Match 100.0%; Score 24; DB 2; Length 237;

Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
|||||
Db 1 LKAMD 5

RESULT 10
JC5709
maleate isomerase (EC 5.2.1.1) - Alcaligenes faecalis
C;Species: Alcaligenes faecalis
C;Date: 03-Dec-1997 #sequence_revision 03-Dec-1997 #text_change 09-Jul-2004
C;Accession: JC5709; PC4412
R;Hatakeyama, K.; Asai, Y.; Uchida, Y.; Kobayashi, M.; Terasawa, M.; Yukawa, H.
Biochem. Biophys. Res. Commun. 239, 74-79, 1997
A;Title: Gene cloning and characterization of maleate cis-trans isomerase from Alcaligenes
A;Reference number: JC5709; MUID:98005083; PMID:9345272
A;Accession: JC5709
A;Molecule type: DNA
A;Residues: 1-253 <HAT>
A;Cross-references: UNIPROT:O24766; DDBJ:AB005051; NID:g2575786; PIDN:BAA23002.1; PID:g2
A;Experimental source: strain IFO 13111
A;Accession: PC4412
A;Molecule type: protein
A;Residues: 1-25 <HA2>
C;Comment: This enzyme catalyzes the conversion of maleate to fumarate.
C;Genetics:
A;Gene: maia
C;Superfamily: Alcaligenes faecalis maleate isomerase
C;Keywords: cis-trans-isomerase

Query Match 100.0%; Score 24; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
|||||
Db 54 LKAMD 58

RESULT 11
C71546
probable glucose-6-phosphate dehydrogenase (devb family) - Chlamydia trachomatis (serotyp
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: C71546
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A;Reference number: A71570; MUID:9900809; PMID:9784136
A;Accession: C71546
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-256 <ARN>
A;Cross-references: UNIPROT:O84189; GB:AE001292; GB:AE001273; NID:g3328586; PIDN:AAC6777
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: devb
C;Superfamily: yeast SOL3 protein

Query Match 100.0%; Score 24; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
|||||
Db 94 LKAMD 98

RESULT 12
CCECID
cell division inhibitor mind - Escherichia coli (strain K-12)

N:Alternate names: septum site-determining protein mind
C:Species: Escherichia coli
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: B31877; D64863
R:De Boer, P.A.J.; Crossley, R.E.; Rothfield, L.I.
Cell 56, 641-649, 1989
A>Title: A division inhibitor and a topological specificity factor coded for by the mind
A:Reference number: A31877; MUID:89136010; PMID:2645057
A:Accession: B31877
A:Molecule type: DNA
A:Residues: 1-270 <DEB>
A:Cross-references: UNIPROT:P18197; GB:J03153; NID:gl46865; PIDN:AAB59062.1; PID:gl46867
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: D64863
A:Molecule type: DNA
A:Residues: 1-270 <BLAT>
A:Cross-references: GB:AE000216; GB:U00096; NID:gl787417; PIDN:AAC74259.1; PID:gl787423;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: mind
A:Map position: 26 min
C:Function:
A>Description: a membrane ATPase required for correct placement of cell division site
A>Note: mind and minC act in concert to form an inhibitor capable of blocking formation
ion found between ftsz and minCD
C:Superfamily: cell division inhibitor mind
C:Keywords: ATP; cell division control; nucleotide binding; P-loop
F:10-17/Region: nucleotide-binding motif A (P-loop)
F:16/Binding site: ATP (Lys) #status Predicted

Query Match 100.0%; Score 24; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
|||||
DB 109 LKAMD 113

RESULT 13
AH0724
septum site determining protein [imported] - Salmonella enterica subsp. enterica serovar
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A>Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AH0724
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Holt, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0724
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-270 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05498.1; PID:gl6503002; GSPDB:GN00176
C:Genetics:
A:Gene: STY1945
C:Superfamily: cell division inhibitor mind

Query Match 100.0%; Score 24; DB 2; Length 270;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
|||||

DB 109 LKAMD 113

RESULT 14
F85695
cell division inhibitor mind - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: F85695
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.; Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dinalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: F85695
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-270 <STO>
A:Cross-references: UNIPROT:P18197; GB:AE005174; NID:gl2514869; PIDN:AAG56026.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: mind
C:Superfamily: cell division inhibitor mind

Query Match 100.0%; Score 24; DB 2; Length 270;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
|||||
DB 109 LKAMD 113

RESULT 15
E90837
cell division inhibitor Mind [imported] - Escherichia coli (strain O157:H7, substrain RI
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: E90837
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E90837
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-270 <HAY>
A:Cross-references: UNIPROT:P18197; GB:BA000007; PIDN:BA035092.1; PID:gl3361133; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs1669
C:Superfamily: cell division inhibitor mind

Query Match 100.0%; Score 24; DB 2; Length 270;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
|||||
DB 109 LKAMD 113

Search completed: May 26, 2005, 18:44:49
Job time : 10.9 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 19:18:07 ; Search time 38.2 Seconds
(without alignments)
67.026 Million cell updates/sec

Title: US-10-047-945-3

Perfect score: 24

Sequence: 1 LKAMD 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	17	2 Q9TR78	Q9tr78 didelphis m
2	24	100.0	52	2 Q27566	Q27566 dictyosteli
3	24	100.0	59	2 Q72NV8	Q72nv8 leptospira
4	24	100.0	62	2 Q72TL6	Q72tl6 leptospira
5	24	100.0	65	2 Q6MJ74	Q6mj74 bdellovibri
6	24	100.0	69	2 Q82KL7	Q82kl7 streptomyce
7	24	100.0	69	2 Q8F7M0	Q8f7m0 leptospira
8	24	100.0	92	2 Q80VT8	Q80vt8 rattus norv
9	24	100.0	98	2 Q8YVG6	Q8yvg6 anabaena sp
10	24	100.0	99	2 Q93CE7	Q93ce7 anabaena va
11	24	100.0	107	2 Q8GU39	Q8gu39 oryza sativ
12	24	100.0	120	2 Q34772	Q34772 synechococc
13	24	100.0	120	2 Q8XJC6	Q8xjc6 clostridium
14	24	100.0	125	2 Q72LB6	Q72lb6 thermus the
15	24	100.0	133	2 Q8EQ29	Q8eqe9 oceanobacil
16	24	100.0	140	2 Q8HZ75	Q8hz75 didelphis m
17	24	100.0	142	2 Q37950	Q37950 lactococcus
18	24	100.0	144	2 Q889V2	Q889v2 pseudomonas
19	24	100.0	144	2 Q88QL6	Q88ql6 pseudomonas
20	24	100.0	144	2 Q9HWF4	Q9hwf4 pseudomonas
21	24	100.0	145	2 Q912X8	Q912x8 pseudomonas
22	24	100.0	166	2 Q655R8	Q655r8 oryza sativ
23	24	100.0	180	2 Q8WMT8	Q8wmt8 eulemur ful
24	24	100.0	180	2 Q8WMT8	Q8wmt8 eulemur ful
25	24	100.0	180	2 Q8WNN7	Q8wnn7 varecia var
26	24	100.0	180	2 Q8WNN8	Q8wnn8 varecia var
27	24	100.0	185	1 LYG CYGAT	P00717 cygnus atra
28	24	100.0	202	2 Q8YH02	Q8yh02 brucella me
29	24	100.0	213	2 Q06732	Q06732 bacillus su
30	24	100.0	226	2 Q9AGS2	Q9age2 streptococc
31	24	100.0	227	2 Q8NIE7	Q8nie7 glomus intr

32 24 100.0 227 2 Q8NJ35 Q8nj35 glomus intr
33 24 100.0 227 2 Q8NJ36 Q8nj36 glomus intr
34 24 100.0 227 2 Q8NJ37 Q8nj37 glomus intr
35 24 100.0 229 2 Q65N09 Q65n09 bacillus li
36 24 100.0 235 2 P93525 P93525 sorghum bic
37 24 100.0 245 2 Q84WD9 Q84wd9 arabidopsis
38 24 100.0 247 2 Q62WWS Q62wWS bacillus li
39 24 100.0 251 2 Q9F155 Q9f155 rhodobacter
40 24 100.0 253 2 Q24766 Q24766 alcaligenes
41 24 100.0 254 2 Q9Z5Q1 Q9z5q1 clostridium
42 24 100.0 256 1 GPGL_CHLMU Q9pkk7 chlamydia m
43 24 100.0 256 1 GPGL_CHLTR Q84l89 chlamydia t
44 24 100.0 256 2 Q65LH4 Q65lh4 bacillus li
45 24 100.0 262 1 FRGI_DROME Q9vwa8 drosophila

ALIGNMENTS

RESULT 1

Q9TR78 PRELIMINARY; PRT; 17 AA.
AC Q9TR78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-BOTHRUPIC complex 48,000 SUBUNIT (Fragment).
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE.
RX MEDLINE=95149299; PubMed=7846694; DOI=10.1016/0041-0101(94)90353-0;
RA Perales J., Mousatche H., Marangoni S., Oliveira B., Domont G.B.;
RT "Isolation and partial characterization of an anti-bothropic complex
from the serum of South American Didelphidae.";
RL Toxicon 32:1237-1249(1994).
SQ SEQUENCE 17 AA; 1947 MW; CB55FB40E73B2A2A CRC64;

Query Match 100.0%; Score 24; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
|||||

Db 1 LKAMD 5

RESULT 2

Q27566 PRELIMINARY; PRT; 52 AA.
AC Q27566;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE UDP-glucose pyrophosphorylase (EC 2.7.7.9) (Fragment).
GN Name=UDPGP2;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA Moon B.-C., Haribabu B., Dottin R.P.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; L28007; AAA91057.1; -.
DR DictyBase; DDB0214911; ugpb.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0003983; F:UTP-glucose-1-phosphate uridylyltransferase. . .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002618; UDPGP_trans.
DR Pfam; PF01704; UDPGP; 1.
KW Nucleotidyltransferase; Transferase.

```

FT  NON TER      1      1
FT  NON TER      52     52
SQ  SEQUENCE     52 AA;  5818 MW;  CCC3C65E75DBA935 CRC64;

Query Match      100.0%; Score 24; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKAMD 5
Db      12 LKAMD 16

RESULT 3
Q72NV8      PRELIMINARY; PRT; 59 AA.
AC Q72NV8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Transposase, IS1533
GN OrderedLocNames=LI12721;
OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
OC Copenhagen).
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=44275;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fiocruz LJ-130;
RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
RA Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeerl R.A.,
RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
RA Coutinho L.L., Degraeve W.M., Dellagostin O.A., El-Dorri H.,
RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglioti E.A.,
RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,
RA Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172(2004).
DR EMBL; AE017297; AAS71278.1; -.
KW Complete proteome.
SQ SEQUENCE 59 AA; 7262 MW; 37037534A845DD90 CRC64;

Query Match      100.0%; Score 24; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKAMD 5
Db      53 LKAMD 57

RESULT 4
Q72TL6      PRELIMINARY; PRT; 62 AA.
AC Q72TL6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Transposase, IS1533
GN OrderedLocNames=LI11002;
OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
OC Copenhagen).
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=44275;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fiocruz LJ-130;

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RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
RA Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeerl R.A.,
RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
RA Coutinho L.L., Degraeve W.M., Dellagostin O.A., El-Dorri H.,
RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglioti E.A.,
RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,
RA Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172(2004).
DR EMBL; AE017291; AAS69612.1; -.
DR InterPro; IPR003346; Transposase_20.
DR Pfam; PF02371; Transposase_20; 1.
KW Complete proteome.
SQ SEQUENCE 62 AA; 7499 MW; C79940D851F0CAC2 CRC64;

Query Match      100.0%; Score 24; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKAMD 5
Db      29 LKAMD 33

RESULT 5
Q6MJ74      PRELIMINARY; PRT; 66 AA.
AC Q6MJ74;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=Bd2909;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL; BX842654; CAE80687.1; -.
KW Complete proteome.
SQ SEQUENCE 66 AA; 8142 MW; 04D5D62C458B6ACD CRC64;

Query Match      100.0%; Score 24; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKAMD 5
Db      21 LKAMD 25

RESULT 6
Q82KL7      PRELIMINARY; PRT; 69 AA.
AC Q82KL7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

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DE Hypothetical protein.
 GN OrderedLocusNames=SAV2586;
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis";
 RL Nat. Biotechnol. 21:526-531(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis; deducing the ability of producing secondary
 RT metabolites";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 DR EMBL; AP005031; BAC70298.1; -.
 KW Complete proteome.
 SQ SEQUENCE 69 AA; 7895 MW; C2E205ASD684D1F8 CRC64;

 Query Match 100.0%; Score 24; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 LKAMD 5
 Db 57 LKAMD 61

 RESULT 7
 ID Q8F7M0 PRELIMINARY; PRT; 69 AA.
 AC Q8F7M0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Transposase.
 GN OrderedLocusNames=LA0924;
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
 RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
 RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
 RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
 RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
 RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
 RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
 RA Xu J.-G., Zhao G.-P.;
 RT "Unique physiological and pathogenic features of Leptospira
 RT interrogans revealed by whole-genome sequencing.";
 RL Nature 422:888-893(2003).
 DR EMBL; AE011276; AAN48123.1; -.
 KW Complete proteome.
 SQ SEQUENCE 69 AA; 8483 MW; 57A13F95666F2504 CRC64;

 Query Match 100.0%; Score 24; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
 Db 63 LKAMD 67

 RESULT 8
 ID Q8OV78 PRELIMINARY; PRT; 92 AA.
 AC Q8OV78;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE S100 calcium-binding protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Ventral prostate;
 RA Oram S.W., Halsem R., Cai X., Cyriac J., Wang Z.;
 RL Submitted (DSC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY195741; AA040742.1; -.
 SQ SEQUENCE 92 AA; 10910 MW; OC406A170449BC19 CRC64;

 Query Match 100.0%; Score 24; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 LKAMD 5
 Db 47 LKAMD 51

 RESULT 9
 ID Q8YVG6 PRELIMINARY; PRT; 98 AA.
 AC Q8YVG6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Acl0884 protein.
 GN OrderedLocusNames=asl0884;
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 DR EMBL; AP003583; BAB72841.1; -.
 DR PIR; A11916; A11916.
 DR HSSP; P21149; IL5P.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR Pfam; PF00111; Fer2; 1.
 KW Complete proteome; Iron; Iron-sulfur; Metal-binding.
 SQ SEQUENCE 98 AA; 10555 MW; 6D2CB4906B92AEE CRC64;

 Query Match 100.0%; Score 24; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
 Db 23 LKAMD 27

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RESULT 10
Q93CE7 PRELIMINARY; PRT; 99 AA.
AC Q93CE7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative.
OS Anabaena variabilis.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=1172;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29413;
RA Schiefer W.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410434; AAL05047.1; -.
DR HSP; P80306; IE9W.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001041; Ferredoxin.
DR Pfam; PF00111; Fer2; 1.
KW Iron; Iron-sulfur; Metal-binding.
SQ SEQUENCE 99 AA; 10702 MW; E3E3CCBA7E8B892A CRC64;

Query Match 100.0%; Score 24; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
Db 23 LKAMD 27

RESULT 11
Q8GU99 PRELIMINARY; PRT; 107 AA.
AC Q8GU99;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MYB29 protein (Fragment).
GN Name=mb29;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu S., Xu Z., Xue H.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ495798; CAD44621.1; -.
DR Gramineae; Q8GU99; -.
FT NON_TER
SQ SEQUENCE 107 AA; 11685 MW; 4899ACD54BE73D98 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
Db 40 LKAMD 44

RESULT 12
Q54772 PRELIMINARY; PRT; 120 AA.
AC Q54772;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Synecococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7942;
RA Phung L.T., Haselkorn R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59237; AAB82030.1; -.
KW Hypothetical protein.
SQ SEQUENCE 120 AA; 13515 MW; 91DDAF420ECFB6B4 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
Db 89 LKAMD 93

RESULT 13
Q8XJC6 PRELIMINARY; PRT; 120 AA.
AC Q8XJC6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein CPE1834.
GN OrderedLocustNames=CPE1834;
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13;
RA MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RX Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RX Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater".
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003192; BAB81540.1; -.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 120 AA; 13909 MW; 063865C7F7FB1632 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
Db 12 LKAMD 16

RESULT 14
Q72LB6 PRELIMINARY; PRT; 125 AA.
AC Q72LB6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical cytosolic protein.
GN OrderedLocustNames=TT00143;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermaceae;
OC Thermus.
OX NCBI_TaxID=262724;

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RN SEQUENCE FROM N.A.
RP PubMed=15064768;
RA Henne A., Brueggemann H., Raasch C., Wierzer A., Hartsch T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacobi C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,
RA Klensk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
RT "The genome sequence of the extreme thermophile Thermus
RT thermophilus."
RL Nat. Biotechnol. 22:547-553(2004).
RL EMBL; AE017301; AAS80491.1; -.
DR InterPro; IPR002744; DUF59.
DR Pfam; PF01883; DUF59; 1.
DR ProDom; PD005595; DUF59; 1.
KW Complete proteome.
SQ SEQUENCE 125 AA; 13658 MW; 77B2D52BCA699896 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
Db 12 LKAMD 16

RESULT 15
Q8QE9 PRELIMINARY; PRT; 133 AA.
AC Q8QE9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytidine-deoxycytidine deaminase (EC 3.5.4.-).
GN Name=cdd; OrderedLocNames=OB1751;
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831;
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments."
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; AP004598; BAC13707.1; -.
DR HSSP; P19079; IJTK.
DR GO; GO:0004126; F:cytidine deaminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0004608; F:cytidine metabolism; IEA.
DR InterPro; IPR006262; Cyt deam tetra.
DR InterPro; IPR002125; dCMP/cyt deam.
DR Pfam; PF00383; dCMP_cyt_deam; 1.
DR TIGRFAMs; TIGR01354; cyt deam tetra; 1.
DR PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 133 AA; 14579 MW; EC56F966FDF4B017 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
Db 11 LKAMD 15

Search completed: May 26, 2005, 18:43:23
Job time : 41.2 secs
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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:17:22 ; Search time 43 Seconds
(without alignments)
44.972 Million cell updates/sec

Title: US-10-047-945-3

Perfect score: 24

Sequence: 1 LKAMD 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	5	2	AAW53842 N-terminu
2	24	100.0	5	7	ABB80224 Synthetic
3	24	100.0	8	7	ABB80228 Synthetic
4	24	100.0	9	7	ABB80227 Synthetic
5	24	100.0	10	2	AAW53843 N-terminu
6	24	100.0	10	7	ABB80222 Synthetic
7	24	100.0	11	7	ABB80226 Synthetic
8	24	100.0	12	7	ABB80225 Synthetic
9	24	100.0	15	2	AAW11575 N-termina
10	24	100.0	15	2	AAW53841 N-terminu
11	24	100.0	15	7	ABB80223 Synthetic
12	24	100.0	42	3	AAW53797 Human col
13	24	100.0	70	3	AAW52152 Human sec
14	24	100.0	70	3	AAW52151 Human sec
15	24	100.0	105	4	ABG12903 Novel hum
16	24	100.0	105	7	ADD29464 Mouse cae
17	24	100.0	112	5	ABP64620 Human ORF
18	24	100.0	141	4	AAW20323 Human pro
19	24	100.0	144	4	AAU33664 Pseudomon
20	24	100.0	144	6	AAU39905 Protein e
21	24	100.0	144	6	ABU42143 Protein e
22	24	100.0	144	6	ABU15537 Protein e
23	24	100.0	145	7	ABO72633 Pseudomon
24	24	100.0	148	4	AAU19728 Human nov
25	24	100.0	148	4	AAU87551 Novel cen

26	24	100.0	148	5	ABP47948 Human pol
27	24	100.0	148	7	ADC10910 Human ext
28	24	100.0	148	8	ADI54866 Novel hum
29	24	100.0	166	4	AAU87251 Novel cen
30	24	100.0	166	8	ADI54566 Novel hum
31	24	100.0	182	7	ABO81340 Pseudomon
32	24	100.0	199	4	AAU87253 Novel cen
33	24	100.0	199	8	ADI54568 Novel hum
34	24	100.0	205	8	ADN17855 Bacterial
35	24	100.0	208	4	AAU19847 Human nov
36	24	100.0	208	4	AAU87553 Novel Cen
37	24	100.0	208	5	ABP48067 Human pol
38	24	100.0	208	7	ADC11029 Human pro
39	24	100.0	208	8	ADI54868 Novel hum
40	24	100.0	212	8	ADSI1888 Human the
41	24	100.0	213	8	ADM87718 Human EST
42	24	100.0	225	7	ADE40152 Human NOV
43	24	100.0	231	8	ADI39310 S. hygro
44	24	100.0	234	8	ADN21642 Bacterial
45	24	100.0	234	8	ADN24398 Bacterial

ALIGNMENTS

RESULT 1

AAW53842
ID AAW53842 standard; peptide; 5 AA.

XX AAW53842;

DT 08-JUL-1998 (first entry)

DE N-terminus of opossum LTNP.

XX LNPF; lethal toxin neutralising factor; opossum; envenomation; therapy;

KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;

KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;

KW histamine reaction treatment.

XX Didelphis virginiana.

OS US5744449-A.

PN 28-APR-1998.

PD 03-JUN-1996; 96US-00657163.

XX 10-MAY-1993; 93US-00058387.

XX 22-SEP-1994; 94US-00310340.

PA (LIPP/) LIPPS B V.

XX (LIPP/) LIPPS F W.

XX Lipps FW, Lipps BV;

XX WPI; 1998-271108/24.

XX Lethal Toxin Neutralising Factor peptide from opossum - can neutralise

PT venom(s) from all major families of poisonous snakes.

XX Claim 5; Col 13; lipp; English.

XX This sequence represents the peptide of the invention. It is a Lethal

CC Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic

CC protein derived from an opossum. The peptide can be used in a method for

CC treating a victim of envenomation from a poisonous snake, preferably a

CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It

CC is useful for the treatment of snake bites, sepsis, allergies caused by

CC the environment and treatment of bee or scorpion stings or toxicities

CC caused by plant or bacterial toxins. The peptide can also be used in

CC histamine reaction treatment. The peptide can be used in envenomation

CC treatment for a variety of snakes without prior identification of the

CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins

XX Sequence 5 AA;
 SQ Query Match 100.0%; Score 24; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKAMD 5
 |||||
 Db 1 LKAMD 5

RESULT 2
 ABB80224
 ID ABB80224 standard; peptide; 5 AA.

XX AC ABB80224;

XX DT 06-NOV-2003 (first entry)

XX DE Synthetic LTNF, LT-5.

XX KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.

XX OS Synthetic.

XX PN WO2003060471-A2.

XX PD 24-JUL-2003.

XX PF 14-JAN-2003; 2003WO-US001044.

XX PR 14-JAN-2002; 2002US-00047945.

XX PA (LIPP/) LIPPS B V.

XX PI (LIPP/) LIPPS F W.

XX PJ Lipps BV, Lipps FW;

XX DR WPI; 2003-636703/60.

XX Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

XX PS Disclosure; Page 3; 24pp; English.

XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX Sequence 5 AA;
 SQ Query Match 100.0%; Score 24; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKAMD 5
 |||||
 Db 1 LKAMD 5

RESULT 3

ABB80228

ID ABB80228 standard; peptide; 8 AA.

XX AC ABB80228;

XX DT 06-NOV-2003 (first entry)

XX DE Synthetic LTNF, LT-8.

XX KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.

XX OS Synthetic.

XX PN WO2003060471-A2.

XX PD 24-JUL-2003.

XX PF 14-JAN-2003; 2003WO-US001044.

XX PR 14-JAN-2002; 2002US-00047945.

XX PA (LIPP/) LIPPS B V.

XX PI (LIPP/) LIPPS F W.

XX PJ Lipps BV, Lipps FW;

XX DR WPI; 2003-636703/60.

XX Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.

XX PS Claim 7; Page 4; 24pp; English.

XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX Sequence 8 AA;

KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.
 XX
 XX WO2003060471-A2.
 XX
 XX 24-JUL-2003.
 XX
 XX 14-JAN-2003; 2003WO-US001044.
 XX
 XX 14-JAN-2002; 2002US-00047945.
 XX
 XX (LIPP/) LIPPS B V.
 XX (LIPP/) LIPPS F W.
 XX
 XX Lipps BV, Lipps FW;
 XX
 XX WPI; 2003-636703/60.
 XX
 XX Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 XX
 PS Claim 7; Page 4; 24pp; English.
 XX
 XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 XX
 XX Sequence 12 AA;
 Query Match 100.0%; Score 24; DB 7; Length 12;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LKAMD 5
 Db 1 LKAMD 5
 RESULT 9
 AAW11575
 ID AAW11575 standard; peptide; 15 AA.
 XX
 XX AAW11575;
 AC
 XX 25-MAR-2003 (revised)
 DT 20-MAR-1997 (first entry)
 XX
 XX N-terminal peptide from lethal toxin neutralising factor.
 XX
 XX Lethal toxin neutralising factor; LTNF; opossum; bee toxin;
 KW scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.

XX Didelphis virginiana.
 OS
 XX US5576297-A.
 PN
 XX 19-NOV-1996.
 PD
 XX 22-SEP-1994; 94US-00310340.
 PF
 XX 10-MAY-1993; 93US-00058387.
 PR
 XX (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.
 PA
 XX Lipps FW, Lipps BV;
 PI
 XX WPI; 1997-011287/01.
 DR
 XX Treatment of victims of bee or scorpion stings or plant or bacterial
 PT toxins - by admin. of lethal toxin-neutralising factor or its N-terminal
 PT peptide.
 PT
 XX Claim 7; Col 9; 9pp; English.
 PS
 XX The present sequence is from the N-terminus of a 68 kD protein purified
 CC from the serum of the opossum *Didelphis virginiana*. The full-length
 CC protein is a lethal toxin neutralising factor (LTNF). The use of purified
 CC LTNF or of the chemically synthesised 15mer N-terminal peptide for
 CC treating victims of bee stings, scorpion stings and bacterial or plant
 CC toxins is claimed. The patent disclosure does not provide any evidence
 CC for neutralising activity against these various toxins. There is evidence
 CC of significant neutralising activity of the opossum LTNF and the 15mer
 CC peptide against venom from snakes of the families Crotalidae, Elapidae,
 CC Hydroliidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)
 CC
 XX Sequence 15 AA;
 Query Match 100.0%; Score 24; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LKAMD 5
 Db 1 LKAMD 5
 RESULT 10
 AAW53841
 ID AAW53841 standard; peptide; 15 AA.
 XX
 XX AAW53841;
 AC
 XX 08-JUL-1998 (first entry)
 DT
 XX N-terminus of opossum LTNF.
 DE
 XX LTNF; lethal toxin neutralising factor; Opossum; envenomation; therapy;
 KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
 KW histamine reaction treatment.
 XX
 XX Didelphis virginiana.
 OS
 XX US5744449-A.
 PN
 XX 28-APR-1998.
 PD
 XX 03-JUN-1996; 96US-00657163.
 PF
 XX 10-MAY-1993; 93US-00058387.
 PR 22-SEP-1994; 94US-00310340.
 XX
 XX (LIPP/) LIPPS B V.

PA (LIPP/) LIPPS F W.
 XX Lipps FW, Lipps BV;
 XX WPI; 1998-271108/24.
 DR Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
 PT venom(s) from all major families of poisonous snakes.
 XX
 XX Claim 1; Col 11; 11pp; English.
 CC This sequence represents the peptide of the invention. It is a lethal
 CC Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic
 CC protein derived from an opossum. The peptide can be used in a method for
 CC treating a victim of envenomation from a poisonous snake, preferably a
 CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
 CC is useful for the treatment of snake bites, sepsis, allergies caused by
 CC the environment and treatment of bee or scorpion stings or toxicities
 CC caused by plant or bacterial toxins. The peptide can also be used in
 CC histamine reaction treatment. The peptide can be used in envenomation
 CC treatment for a variety of snakes without prior identification of the
 CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 24; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMD 5
 DB 1 LKAMD 5
 RESULT 11
 ABB80223
 ID ABB80223 standard; peptide; 15 AA.
 XX
 AC ABB80223;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Synthetic LTNP, LT-15.
 XX
 KW Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.
 XX
 PN WO2003060471-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 14-JAN-2003; 2003WO-US001044.
 XX
 PR 14-JAN-2002; 2002US-00047945.
 XX
 PA (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.
 XX
 PI Lipps BV, Lipps FW;
 XX
 DR WPI; 2003-636703/60.
 XX
 XX Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a

PT patient.
 XX
 PS Claim 3; Page 3; 24pp; English.
 XX
 CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 24; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMD 5
 DB 1 LKAMD 5
 RESULT 12
 AAB53797
 ID AAB53797 standard; protein; 42 AA.
 XX
 AC AAB53797;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DE Human colon cancer antigen protein sequence SEQ ID NO:1337.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnary;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; antifibrotic; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200055351-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US005883.
 XX
 PR 12-MAR-1999; 99US-0124270P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2000-587534/55.
 DR N-PSDB; AAC98554.
 XX
 XX Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer.
 XX
 PS Claim 11; Page 1918; 2104pp; English.

XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal, and
 CC vulnary, nephrotropic, antineoplastic and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins may
 CC also be used to prevent diseases such as neural disorders, immune system
 CC disorders, muscular disorders, reproductive disorders, gastrointestinal
 CC disorders, wounds, renal disorders, infectious diseases, and
 CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
 CC sequences used in the exemplification of the present invention
 XX
 SQ Sequence 42 AA;

Query Match 100.0%; Score 24; DB 3; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
 Db 28 LKAMD 32

RESULT 13
 AAB52152
 ID AAB52152 standard; protein; 70 AA.

AC AAB52152;
 DT 22-FEB-2001 (first entry)

DE Human secreted protein BLAST search protein SEQ ID NO: 108.

XX Cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.

XX Homo sapiens.

XX WO200061624-A1.

XX 19-OCT-2000.

XX 06-APR-2000; 2000WO-US008980.

XX 09-APR-1999; 99US-0128700P.

XX 20-JAN-2000; 2000US-0176930P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI; 2000-656324/63.

XX New nucleic acid molecules encoding human secreted proteins, used in
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
 PT Parkinson's diseases and cancers.

XX Disclosure; Page 447; 478pp; English.

XX The invention relates to the isolation of genes AAC96900-C96947 encoding
 CC the human secreted proteins AAB52104-B52150. This sequence was used as a
 CC query sequence for BLASTX searches. The genes and proteins are useful for
 CC preventing, ameliorating or treating medical conditions, e.g. by protein
 CC or gene therapy. The genes are isolated from a range of human tissues
 CC disclosed in the specification. The nucleic acids, proteins, antibodies

CC and (ant)agonists are useful in the diagnosis, treatment and prevention
 CC of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
 CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
 CC myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g.
 CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
 CC bacterial, fungal and parasitic infections
 XX
 SQ Sequence 70 AA;

Query Match 100.0%; Score 24; DB 3; Length 70;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
 Db 16 LKAMD 20

RESULT 14

AAB52151
 ID AAB52151 standard; protein; 70 AA.

XX AAB52151;

DT 22-FEB-2001 (first entry)

DE Human secreted protein BLAST search protein SEQ ID NO: 107.

XX Cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.

XX Homo sapiens.

XX WO200061624-A1.

XX 19-OCT-2000.

XX 06-APR-2000; 2000WO-US008980.

XX 09-APR-1999; 99US-0128700P.

XX 20-JAN-2000; 2000US-0176930P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI; 2000-656324/63.

XX New nucleic acid molecules encoding human secreted proteins, used in
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
 PT Parkinson's diseases and cancers.

XX Disclosure; Page 446; 478pp; English.

XX The invention relates to the isolation of genes AAC96900-C96947 encoding
 CC the human secreted proteins AAB52104-B52150. This sequence is a search
 CC result from a BLASTX homology search. The genes and proteins are useful
 CC for preventing, ameliorating or treating medical conditions, e.g. by
 CC protein or gene therapy. The genes are isolated from a range of human
 CC tissues disclosed in the specification. The nucleic acids, proteins,
 CC antibodies and (ant)agonists are useful in the diagnosis, treatment and
 CC prevention of: (a) cancer, e.g. breast and ovarian cancer, and other
 CC cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal
 CC tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's
 CC disease, allergies, autoimmune haemolytic anaemia, autoimmune
 CC thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis,

CC rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders
 CC such as myocardial ischemias; (d) wound healing; (e) neurological
 CC diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases
 CC such as viral, bacterial, fungal and parasitic infections

XX SQ Sequence 70 AA;

Query Match 100.0%; Score 24; DB 3; Length 70;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

Qy 1 LKAMD 5
 |||||
 Db 16 LKAMD 20

RESULT 15

ABG12903
 ID ABG12903 standard; protein; 105 AA.

XX AC ABG12903;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #12894.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSEQ-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR N-PSDB; AAS77090.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20; SEQ ID NO 43262; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG0377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 105 AA;

Query Match 100.0%; Score 24; DB 4; Length 105;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
 |||||
 Db 29 LKAMD 33

Search completed: May 26, 2005, 18:36:55
 Job time : 46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2005, 18:43:39 ; Search time 32.8 Seconds
(without alignments)
52.587 Million cell updates/sec

Title: US-10-047-945-3

Perfect score: 24

Sequence: 1 LKAMD 5

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*

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17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	24	100.0	9	14	US-10-047-945-6
4	24	100.0	10	14	US-10-047-945-1
5	24	100.0	11	14	US-10-047-945-5
6	24	100.0	12	14	US-10-047-945-4
7	24	100.0	15	14	US-10-047-945-2
8	24	100.0	42	9	US-09-925-299-1337
9	24	100.0	42	10	US-09-925-299-1337
10	24	100.0	69	14	US-10-156-761-10123
11	24	100.0	70	15	US-10-424-599-187934
12	24	100.0	86	15	US-10-424-599-148579
13	24	100.0	98	16	US-10-767-701-41212

14	24	100.0	103	16	US-10-767-701-34493	Sequence 34493, A
15	24	100.0	105	15	US-10-449-857A-40	Sequence 40, Appl
16	24	100.0	112	9	US-09-867-550-1980	Sequence 1980, Ap
17	24	100.0	126	15	US-10-424-599-275786	Sequence 275786,
18	24	100.0	127	15	US-10-424-599-183694	Sequence 183694,
19	24	100.0	144	9	US-09-815-242-5160	Sequence 5160, Ap
20	24	100.0	144	15	US-10-282-122A-43461	Sequence 43461, A
21	24	100.0	144	15	US-10-282-122A-67829	Sequence 67829, A
22	24	100.0	144	15	US-10-282-122A-70067	Sequence 70067, A
23	24	100.0	148	9	US-09-764-870-378	Sequence 378, App
24	24	100.0	148	11	US-09-764-875-1069	Sequence 1069, Ap
25	24	100.0	148	14	US-10-125-540-378	Sequence 378, App
26	24	100.0	151	17	US-10-732-923-9567	Sequence 9567, Ap
27	24	100.0	166	11	US-09-764-875-769	Sequence 769, App
28	24	100.0	199	11	US-09-764-875-771	Sequence 771, App
29	24	100.0	205	15	US-10-369-493-508	Sequence 508, App
30	24	100.0	208	9	US-09-764-870-497	Sequence 497, App
31	24	100.0	208	11	US-09-764-875-1071	Sequence 1071, Ap
32	24	100.0	208	14	US-10-125-540-497	Sequence 497, App
33	24	100.0	213	15	US-10-112-944-811	Sequence 811, App
34	24	100.0	225	15	US-10-210-172-58	Sequence 70803, A
35	24	100.0	230	15	US-10-425-114-70803	Sequence 152, App
36	24	100.0	231	15	US-10-461-194-152	Sequence 4295, Ap
37	24	100.0	234	15	US-10-369-493-4295	Sequence 4295, Ap
38	24	100.0	234	15	US-10-369-493-7051	Sequence 7051, Ap
39	24	100.0	234	17	US-10-965-898-35	Sequence 35, Appl
40	24	100.0	239	11	US-09-764-875-665	Sequence 665, App
41	24	100.0	244	15	US-10-424-599-154522	Sequence 154522,
42	24	100.0	244	16	US-10-767-701-43262	Sequence 43262, A
43	24	100.0	270	13	US-10-067-989-4	Sequence 4, Appli
44	24	100.0	272	10	US-09-769-787-71	Sequence 71, Appl
45	24	100.0	272	15	US-10-282-122A-74006	Sequence 74006, A

ALIGNMENTS

RESULT 1

US-10-047-945-3

; Sequence 3, Application US/10047945

; Publication No. US20030157555A1

; GENERAL INFORMATION:

; APPLICANT: LIPPS, BINIE V.

; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

; TITLE OF INVENTION: (IGE)IMPLICATED DISORDERS

; FILE REFERENCE: FWPAT015US

; CURRENT APPLICATION NUMBER: US/10/047,945

; PRIOR FILING DATE: 2002-01-14

; PRIOR APPLICATION NUMBER:

; PRIOR FILING DATE:

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

; SEQ ID NO 3

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY:

; LOCATION:

; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM

; OTHER INFORMATION: US 5,576,297.

US-10-047-945-3

Query Match 100.0%; Score 24; DB 14; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.3e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 LKAMD 5

|||||

1 LKAMD 5

Db

RESULT 2
US-10-047-945-7
; Sequence 7, Application US/10047945
; Publication No. US20030157555A1

; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.

US-10-047-945-7

Query Match 100.0%; Score 24; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
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|
DB 1 LKAMD 5

RESULT 3
US-10-047-945-6
; Sequence 6, Application US/10047945
; Publication No. US20030157555A1

; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.

US-10-047-945-6

Query Match 100.0%; Score 24; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
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|
DB 1 LKAMD 5

RESULT 4
US-10-047-945-1
; Sequence 1, Application US/10047945

; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-1

Query Match 100.0%; Score 24; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
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|
|
|
DB 1 LKAMD 5

RESULT 5
US-10-047-945-5
; Sequence 5, Application US/10047945
; Publication No. US20030157555A1

; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.

US-10-047-945-5

Query Match 100.0%; Score 24; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
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|
|
|
DB 1 LKAMD 5

RESULT 6
US-10-047-945-4
; Sequence 4, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:

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; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1337
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (23)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (34)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (40)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-925-299-1337
;
Query Match          100.0%; Score 24; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LKAMD 5
DB      28 LKAMD 32
      |||||

RESULT 9
US-09-925-299-1337
; Sequence 1337, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1337
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

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; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (23)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (34)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (40)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1337

Query Match 100.0%; Score 24; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
Db 28 LKAMD 32

RESULT 10
US-10-156-761-10123
; Sequence 10123, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10123
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10123

Query Match 100.0%; Score 24; DB 14; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
Db 57 LKAMD 61

RESULT 11
US-10-424-599-187934
; Sequence 187934, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701

; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 187934
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(70)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_140719C.1.pep
US-10-424-599-187934

Query Match 100.0%; Score 24; DB 15; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
Db 23 LKAMD 27

RESULT 12
US-10-424-599-148579
; Sequence 148579, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 148579
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(86)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_105189C.1.pep
US-10-424-599-148579

Query Match 100.0%; Score 24; DB 15; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
Db 5 LKAMD 9

RESULT 13
US-10-767-701-41212
; Sequence 41212, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701


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; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 41212
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C26778_1.pep
US-10-767-701-41212

Query Match      100.0%; Score 24; DB 16; Length 98;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LKAMD 5
Db      30 LKAMD 34

RESULT 14
US-10-767-701-34493
; Sequence 34493, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10767.701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 34493
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49505_1.pep
US-10-767-701-34493

Query Match      100.0%; Score 24; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LKAMD 5
Db      54 LKAMD 58

RESULT 15
US-10-449-857A-40
; Sequence 40, Application US/10449857A
; Publication No. US20040043931A1
; GENERAL INFORMATION:
; APPLICANT: Hersberg, Robert M.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 584C1
; CURRENT APPLICATION NUMBER: US/10/449.857A
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 40
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Unknown Bacterium
US-10-449-857A-40
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Query Match      100.0%; Score 24; DB 15; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LKAMD 5
Db      12 LKAMD 16
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Search completed: May 26, 2005, 19:17:35
Job time : 54.8 secs

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ORIGINAL SOURCE: SYNTHETIC
US-08-657-163A-3

Query Match 100.0%; Score 24; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
|
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|
|
Db 1 LKAMD 5

RESULT 2
US-08-657-163A-2
; Sequence 2, Application US/08657163A
; Patent No. 5744449
; GENERAL INFORMATION:
; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
; TITLE OF INVENTION: SYNTHETIC LIPIDS AND THEIR
; TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BINIE V. LIPPS
; STREET: 4509 MIMOSA DR.
; CITY: BELLAIRE
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
; SOFTWARE: MS WORD 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,163A
; FILING DATE: 22 SEPTEMBER 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,340
; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN R. CASPERSON
; REGISTRATION NUMBER: 28,198
; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-482-2961
; TELEFAX: 713-663-7290
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N
; ORIGINAL SOURCE: SYNTHETIC
US-08-657-163A-2

Query Match 100.0%; Score 24; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
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|
|
|
Db 1 LKAMD 5

RESULT 3
US-08-310-340A-1
; Sequence 1, Application US/08310340A
; Patent No. 5576297
; GENERAL INFORMATION:
; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
; TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR
; TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BINIE V. LIPPS
; STREET: 4509 MIMOSA DR.
; CITY: BELLAIRE
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
; SOFTWARE: MS WORD 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,340A
; FILING DATE: 22 SEPTEMBER 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/058, 387
; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-723-6845
; TELEFAX: 713-663-7290
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N
; ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
; ORGANISM: DIBELPHIS VIRGINIANA
; STRAIN: WILD
; INDIVIDUAL ISOLATE: TEXAS WILD
; DEVELOPMENTAL STAGE: ADULT
; HAPLOTYPE:
; TISSUE TYPE: BLOOD
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
; LIBRARY:
; CLONE:
; PUBLICATION INFORMATION:
; AUTHORS: JONAS PERALES, ET AL.
; TITLE: ANTI-SNAKE VENOM FORM DIBELPHIDAE
; JOURNAL: INTERNATIONAL SOCIETY ON
; JOURNAL: TOXINOLOGY
; VOLUME: 10TH WORLD CONGRESS ON ANIMAL
; VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
; VOLUME: SINGAPORE
; ISSUE: PROGRAMME AND ABSTRACTS
; PAGES: 104
; DATE: 3-8 NOV 1991
US-08-310-340A-1

Query Match 100.0%; Score 24; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
Db 1 LKAMD 5

RESULT 4
US-08-657-163A-1
; Sequence 1, Application US/08657163A
; Patent No. 574449
; GENERAL INFORMATION:
; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
; TITLE OF INVENTION: SYNTHETIC LIPNS AND THEIR
; TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BINIE V. LIPPS
; STREET: 4509 MIMOSA DR.
; CITY: BELLAIRE
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77401

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
; SOFTWARE: MS WORD 2.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,163A
; FILING DATE:

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,340

; FILING DATE: 22 SEPTEMBER 1994
; CLASSIFICATION: 514
; APPLICATION NUMBER: 08/058,387

; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN R. CASPERSON

; REGISTRATION NUMBER: 28,198
; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
; TELEPHONE: 713-482-2961

; TELEFAX: 713-663-7290
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
; HYPOTHETICAL: NO

; ANTI-SENSE: NO
; FRAGMENT TYPE: N
; ORIGINAL SOURCE: OPOSSUM SERA; SEQ ID NO: 1:

; ORGANISM: DIDELEPHIS VIRGINIANA
; STRAIN: WILD
; INDIVIDUAL ISOLATE: TEXAS WILD

; DEVELOPMENTAL STAGE: ADULT
; HAPLOTYPE:
; TISSUE TYPE: BLOOD

; CELL TYPE:
; CELL LINE:
; ORGANELLE:

; IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
; LIBRARY:
; CLONE:

; PUBLICATION INFORMATION:
; AUTHORS: JONAS PERALES, ET AL.
; TITLE: ANTI-SNAKE VENOM FORM DIDELEPHIDAE
; JOURNAL: INTERNATIONAL SOCIETY ON
; JOURNAL: TOXICOLOGY
; VOLUME: 10TH WORLD CONGRESS ON ANIMAL
; VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
; ISSUE: PROGRAMME AND ABSTRACTS
; PAGES: 104
; DATE: 3-8 NOV 1991
; US-08-657-163A-1

Query Match 100.0%; Score 24; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
Db 1 LKAMD 5

RESULT 5
US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
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; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
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; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
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; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
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; Patent No. 6551795
; GENERAL INFORMATION:
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; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
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; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21379
; Sequence 21379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21379
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

QY 1 LKAMD 5
|||||
Db 17 LKAMD 21

RESULT 7

US-09-270-767-33745
; Sequence 33745, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 33745

; LENGTH: 174

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-33745

Query Match

Best Local Similarity 100.0%; Score 24; DB 4; Length 174;

Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
|||||
Db 31 LKAMD 35

RESULT 8

US-09-270-767-48962

; Sequence 48962, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 48962

; LENGTH: 174

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-48962

Query Match

Best Local Similarity 100.0%; Score 24; DB 4; Length 174;

Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
|||||
Db 31 LKAMD 35

RESULT 9

US-09-252-991A-30086

; Sequence 30086, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30086
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30086

Query Match 100.0%; Score 24; DB 4; Length 182;
Best Local Similarity 100.0%; Pred. No. 89;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
|||||
Db 59 LKAMD 63

RESULT 10

US-09-949-016-7062

; Sequence 7062, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7062

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-7062

Query Match 100.0%; Score 24; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 95;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
|||||
Db 2 LKAMD 6

RESULT 11

US-09-949-016-8959

; Sequence 8959, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8959

; LENGTH: 192

TYPE: PRT
ORGANISM: Human
US-09-949-016-8959

Query Match 100.0%; Score 24; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
Db 2 LKAMD 6

RESULT 12

US-09-949-016-11113
; Sequence 11113, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11113
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11113

Query Match 100.0%; Score 24; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
Db 2 LKAMD 6

RESULT 13

US-09-248-796A-25133
; Sequence 25133, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 25133
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-25133

Query Match 100.0%; Score 24; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
Db 111 LKAMD 115

RESULT 14

US-09-583-110-4560
; Sequence 4560, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; PNEUMONIAE for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4560
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4560

Query Match 100.0%; Score 24; DB 4; Length 272;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMD 5
Db 48 LKAMD 52

RESULT 15

US-09-107-433-4420
; Sequence 4420, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4420:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...284
SEQUENCE DESCRIPTION: SEQ ID NO: 4420:
US-09-107-433-4420

Query Match 100.0%; Score 24; DB 4; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMD 5
Db 60 LKAMD 64

Search completed: May 26, 2005, 19:08:39
Job time : 12.6 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:26:23 ; Search time 18.96 Seconds
(without alignments)
60.897 Million cell updates/sec

Title: US-10-047-945-4
Perfect score: 69
Sequence: 1 LKAMDPTPLWI 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	75.4	237	2 A42013	alpha-1-B-glycoprotein
2	43	62.3	695	2 E75099	hypothetical prote
3	43	62.3	932	1 A31898	hydroxymethylgluta
4	43	62.3	1213	2 A54063	TATA-binding prote
5	42	60.9	115	2 D71194	hypothetical prote
6	42	60.9	398	2 A81717	conserved hypothet
7	42	60.9	662	2 A29900	fasciclin I precur
8	42	60.9	1327	2 T09402	immunoglobulin-lik
9	41	59.4	707	2 F86925	probable acyl-CoA
10	41	59.4	967	2 S58360	antibiotic peps b
11	40	58.0	205	2 S26894	microfilarial sheat
12	40	58.0	205	2 A40525	proline-rich sheat
13	40	58.0	225	2 C70045	two-component resp
14	40	58.0	406	2 C83867	Xaa-Pro dipeptidas
15	40	58.0	560	2 T02404	probable beta-gluc
16	40	58.0	609	2 S65208	probable membrane
17	39.5	57.2	365	2 F87552	dprA protein [impo
18	39	56.5	268	2 S31010	gene 65 protein -
19	39	56.5	426	2 T16406	hypothetical prote
20	39	56.5	492	2 T16659	hypothetical prote
21	39	56.5	564	1 VHXPV	major structural n
22	39	56.5	663	1 A69798	beta-galactosidase
23	39	56.5	1212	2 D88175	protein T24H7.5a [
24	39	56.5	1215	2 E70614	hypothetical prote
25	39	56.5	1454	2 C88175	protein T24H7.5b [
26	39	56.5	1728	2 T17466	rifamycin polyketi
27	38.5	55.8	401	1 REMSS	renin (EC 3.4.23.1
28	38.5	55.8	402	1 REMSK	renin (EC 3.4.23.1
29	38	55.1	259	2 C71820	hypothetical prote

30	38	55.1	347	2 B70710	hypothetical prote
31	38	55.1	364	2 T10945	peroxidase (EC 1.1
32	38	55.1	660	2 T22794	hypothetical prote
33	38	55.1	792	2 T29187	hypothetical prote
34	38	55.1	896	2 C85438	hypothetical prote
35	38	55.1	1127	2 E97580	hypothetical prote
36	38	55.1	1325	2 S62497	probable nucleopor
37	38	55.1	1443	2 S05979	steroid hormone re
38	37.5	54.3	1145	2 T33606	hypothetical prote
39	37	53.6	86	2 AB2368	hypothetical prote
40	37	53.6	116	2 G72520	hypothetical prote
41	37	53.6	142	2 AE1681	similar o transcri
42	37	53.6	144	2 AG2568	hypothetical prote
43	37	53.6	149	2 A83045	hypothetical prote
44	37	53.6	162	2 C70829	hypothetical prote
45	37	53.6	212	2 C87585	hypothetical prote

ALIGNMENTS

RESULT 1

A42013

alpha-1-B-glycoprotein - North American opossum (fragments)

C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)

C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004

C;Accession: A42013

R;Catanesse, J.J.; Kress, L.P.

Biochemistry 31, 410-418, 1992

A;Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hum

A;Reference number: A42013; MUID:92118834; PMID:1731898

A;Accession: A42013

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-237 <CAT>

A;Cross-references: UNIPROT:Q28359; GB:J05356

C;Keywords: glycoprotein

Query Match 75.4%; Score 52; DB 2; Length 237;
Best Local Similarity 83.3%; Pred. No. 0.26;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWI 12

Db 1 LKAMDPTPLWI 12

RESULT 2

E75099

hypothetical protein PAB1590 - Pyrococcus abyssi (strain Orsay)

C;Species: Pyrococcus abyssi

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C;Accession: E75099

R;anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru

A;Reference number: A75001

A;Accession: E75099

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-695 <KAW>

A;Cross-references: UNIPROT:Q9U2G1; GB:AJ248286; GB:AL096836; NID:G5458366; PIDN:CAB5009

A;Experimental source: strain Orsay

C;Genetics:

A;Gene: PAB1590

Query Match 62.3%; Score 43; DB 2; Length 695;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AMDPTPLWI 12

Db 561 ANDPKPML 570

A;Reference number: A94202; MUID:88276943; PMID:2839842
A;Accession: A31817
A;Molecule type: mRNA
A;Residues: 25-42 <SNO>
A;Cross-references: EMBL:M20544; EMBL:J03787

Query Match 60.9%; Score 42; DB 2; Length 662;
Best Local Similarity 58.3%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPLW 12
| : | | | | |
Db 104 LSELDGNPPLW 115

RESULT 8

T09402

immunoglobulin-like protein IGSF1 - human

C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
A;Accession: T09402
R;Mazzarella, R.; Pengu, G.; Jones, J.; Jones, C.; Schlessinger, D.

Genomics 48, 157-162, 1998

A;Title: Cloning and expression of an immunoglobulin superfamily gene (IGSF1) in Xq25.

A;Reference number: Z16665; MUID:98190514; PMID:9521868

A;Accession: T09402

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1327 <MAZ>

A;Cross-references: UNIPROT:O15070; EMBL:AF034198; NID:g2645889; PIDN:AAC52057.1; PID:g2

C;Genetics:

A;Gene: igsf1

A;Map position: Xq25

Query Match 60.9%; Score 42; DB 2; Length 1327;

Best Local Similarity 77.8%; Pred. No. 84;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MDPTPPLW 12

| | | | |

Db 25 MDQPELW 33

RESULT 9

F86925

Probable acyl-CoA synthetase [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C;Accession: F86925

R;Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A;Title: Massive gene decay in the leprosy bacillus.

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: F86925

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-707 <STO>

A;Cross-references: UNIPROT:Q9CD82; GB:AL450380; NID:gl3092512; PIDN:CAC29642.1; GSPDB:G

C;Genetics:

A;Gene: fadD22

Query Match 59.4%; Score 41; DB 2; Length 707;

Best Local Similarity 54.5%; Pred. No. 61;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPLW 11

| : | | | | |

Db 486 LRAQSPTKPIW 496

RESULT 10

S58360

lambiotic Pep5 biosynthesis protein pepB - Staphylococcus epidermidis

C;Species: Staphylococcus epidermidis

C;Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C;Accession: S66655; S58360

R;Meyer, C.; Bierbaum, G.; Heidrich, C.; Reis, M.; Sueling, J.; Iglesias-Wind, M.I.; Kem

Eur. J. Biochem. 232, 478-489, 1995

A;Title: Nucleotide sequence of the lambiotic Pep5 biosynthetic gene cluster and funct

A;Reference number: S66651; MUID:96035882; PMID:7556197

A;Accession: S66655

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-967 <ME2>

A;Cross-references: UNIPROT:Q54123; EMBL:Z49865; NID:G945014; PIDN:CAA90025.1; PID:G9450

C;Genetics:

A;Gene: pepB

C;Keywords: antibiotic biosynthesis

Query Match 59.4%; Score 41; DB 2; Length 967;

Best Local Similarity 54.5%; Pred. No. 87;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPLW 11

: | | | | |

Db 102 IKALDTTNPW 112

RESULT 11

S26854

microfilarial sheath protein, major component - nematode (Brugia pahangi)

C;Species: Brugia pahangi

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S26854

R;Selkirk, M.

submitted to the EMBL Data Library, February 1991

A;Reference number: S26854

A;Accession: S26854

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-205 <SEL>

A;Cross-references: UNIPROT:Q00032; EMBL:X58063; NID:G5951; PID:G5952

C;Genetics:

A;Introns: 123/2

Query Match 58.0%; Score 40; DB 2; Length 205;

Best Local Similarity 54.5%; Pred. No. 23;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPLW 11

| | | | |

Db 146 LTQOTPTPPIW 156

RESULT 12

A40525

proline-rich sheath protein Mf22 precursor - nematode (Brugia pahangi)

C;Species: Brugia pahangi

C;Date: 28-Feb-1992 #sequence_revision 10-Apr-1992 #text_change 09-Jul-2004

C;Accession: A40525; S18744

R;Selkirk, M.E.; Yazdankhah, M.; Freedman, D.; Blaxter, M.L.; Cookson, E.; Jenkins, R.

J. Biol. Chem. 266, 11002-11008, 1991

A;Title: A proline-rich structural protein of the surface sheath of larval Brugia filari

A;Reference number: A40525; MUID:91250404; PMID:1710216

A;Accession: A40525

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-205 <SEL>

A;Cross-references: UNIPROT:Q00032; GB:X58063

A;Note: the authors translated the codon GCA for residue 23 as Arg, CTG for residue 146

Query Match 58.0%; Score 40; DB 2; Length 205;

Best Local Similarity 54.5%; Pred. No. 23;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPLW 11
| | | | |
Db 146 LTQQTPTPIW 156

RESULT 13
C70045
two-component response regulator [YvqB] homolog yvqA - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: C70045
R:Kunz, S.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C:Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A: Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Puma, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidine, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y. M.; Ogawa, K.; Ogihara, K.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Togononi, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: C70045
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-225 <KUN>
A:Cross-references: UNIPROT:Q32192; GB:Z99120; GB:AL009126; NID:g2635613; PIDN:CB15291.
A:Experimental source: strain 168
C:Genetics:
A:Gene: yvqA
C:Superfamily: ompR protein; response regulator homology
C:Keywords: phosphoprotein
F:5-113/Domain: response regulator homology <RRH>
F:52/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 58.0%; Score 40; DB 2; Length 225;
Best Local Similarity 63.6%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAMDPTPLW 12
| | | | |
Db 40 KMTSPHLW 50

RESULT 14
C83867
Xaa-Pro dipeptidase BH1739 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: C83867
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: C83867
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <STO>
A:Cross-references: UNIPROT:Q9KC35; GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BA8054
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1739

Query Match 58.0%; Score 40; DB 2; Length 406;
Best Local Similarity 71.4%; Pred. No. 49;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 PTPPLW 12
| | | | |
Db 389 PSPPLWV 395

RESULT 15

T02404

probable beta-glucosidase homolog F411.30 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004

C:Accession: T02404; B84879

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

submitted to the EMBL Data Library, May 1998

A:Description: Arabidopsis thaliana chromosome II BAC F411 genomic sequence.

A:Reference number: Z14667

A:Accession: T02404

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-560 <ROU>

A:Cross-references: UNIPROT:O64883; EMBL:AC004521; NID:g3128166; PIDN:AAC16095.1; PID:g3

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: B84879

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-560 <STO>

A:Cross-references: GB:AE002093; NID:g3128191; PIDN:AAC16095.1; GSPDB:GNO0139

C:Genetics:

A:Gene: At2g44490; F411.30

A:Map position: 2

A:Introns: 3/2; 33/3; 76/3; 102/1; 157/2; 242/3; 281/2; 354/1; 400/1; 438/2

C:Superfamily: Agrobacterium beta-glucosidase

Query Match 58.0%; Score 40; DB 2; Length 560;
Best Local Similarity 54.5%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKAMDPTPLW 11
| | | | |
Db 334 IKQVDTQPTW 344

Search completed: May 26, 2005, 18:44:50

Job time : 19.96 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:18:07 ; Search time 91.68 Seconds
(without alignments)
67.026 Million cell updates/sec

Title: US-10-047-945-4

Perfect score: 69

Sequence: 1 LKAMDPTPLWI.12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	17	Q9TR78	Q9tr78 didelphis m
2	69	100.0	291	DM43 DIDMR	P82957 didelphis m
3	60	87.0	140	Q8HZ75	Q8hz75 didelphis m
4	60	87.0	291	Q8HZ74	Q8hz74 didelphis m
5	52	75.4	314	Q8HYX5	Q8hyx5 didelphis m
6	50	72.5	227	Q73ZB2	Q73zb2 mycobacteri
7	46	66.7	370	Q7QE48	Q7qe48 anopheles g
8	45	65.2	128	Q833V1	Q833v1 enterococcu
9	45	65.2	467	Q7YQJ7	Q7yqj7 sus scrofa
10	44	63.8	242	Q8BXK6	Q8bxk6 mus musculu
11	44	63.8	477	Q18150	Q18150 caenorhabdi
12	43	62.3	351	Y4VJ RHISN	Q53218 rhizobium s
13	43	62.3	354	Q8VM74	Q8vm74 rhizobium s
14	43	62.3	360	Q846T8	Q846t8 myxococcus
15	43	62.3	695	Q9UZG1	Q9uzg1 pyrococcus
16	43	62.3	932	HWDH_STRPU	P16391 strongyloce
17	43	62.3	1221	TF22 DROME	Q4325 drosophila
18	42	60.9	115	Q59492	O59492 pyrococcus
19	42	60.9	190	Q7Q324	Q7q324 anopheles g
20	42	60.9	242	Q8N6C5	Q8n6c5 homo sapien
21	42	60.9	356	Q6FB99	Q6fb99 acinetobact
22	42	60.9	398	Y306 CHLMU	Q9pl02 chlamydia m
23	42	60.9	408	Q7WLE6	Q7wle6 bordetella
24	42	60.9	576	Q6YID6	Q6yid6 penaeus mon
25	42	60.9	612	Q83WX7	Q83wx7 streptomyce
26	42	60.9	662	1 FAS1 SCHAM	P10675 schistocerc
27	42	60.9	1437	Q15070	O15070 homo sapien
28	41	59.4	51	Q8FNB0	Q8fnb0 corynebact
29	41	59.4	99	Q6CS47	Q6cs47 kluyveromyc
30	41	59.4	125	Q9NV61	Q9nv61 homo sapien
31	41	59.4	165	Q9W3H5	Q9w3h5 drosophila

32 41 59.4 212 2 Q6UW07 Q6uw07 homo sapien
33 41 59.4 222 2 Q9HBJ8 Q9hbj8 homo sapien
34 41 59.4 344 2 Q7MTQ9 Q7mtq9 porphyromon
35 41 59.4 504 2 Q8MIS3 Q8mis3 didelphis m
36 41 59.4 634 2 Q9VQP3 Q9vqp3 drosophila
37 41 59.4 707 2 Q9CD82 Q9cd82 mycobacteri
38 41 59.4 854 2 Q9VQP4 Q9vqp4 drosophila
39 41 59.4 856 2 Q9GZ10 Q9gz10 drosophila
40 41 59.4 967 2 Q54123 Q54123 staphylococ
41 41 59.4 1017 2 Q7KU30 Q7ku30 drosophila
42 41 59.4 1305 1 RRPL_AHSV9
43 40 58.0 78 2 Q7NFI1 Q7nfi1 gloebacter
44 40 58.0 137 2 Q6UXU0 Q6uxu0 homo sapien
45 40 58.0 205 2 Q00032 Q00032 brugia pana

ALIGNMENTS

RESULT 1

Q9TR78 PRELIMINARY; PRT; 17 AA.
AC Q9TR78;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ANTI-BOTHRPIC complex 48,000 SUBUNIT (Fragment).
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE.
RX MEDLINE=95149299; PubMed=7846694; DOI=10.1016/0041-0101(94)90353-0;
RA Perales J., Mousatche H., Marangoni S., Oliveira B., Domont G.B.;
RT "Isolation and partial characterization of an anti-bothropic complex
from the serum of South American Didelphidae.";
RL Toxicol 32:1237-1249(1994).
SQ SEQUENCE 17 AA; 1947 MW; CB55FB40E73B2A2A CRC64;

Query Match 100.0%; Score 69; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00027;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWI 12

Db 1 LKAMDPTPLWI 12

RESULT 2

DM43 DIDMR STANDARD; PRT; 291 AA.
AC P82957;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom metalloproteinase inhibitor DM43.
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Serum;
RX MEDLINE=21933368; PubMed=11815628; DOI=10.1074/jbc.M200589200;
RA Neves-Ferreira A.G.C., Perales J., Fox J.W., Shannon J.D.,
RA Makino D.I., Garratt R.C., Domont G.B.;
RT "Structural and functional analyses of DM43, a snake venom
metalloproteinase inhibitor from Didelphis marsupialis serum.";
RL J. Biol. Chem. 277:13129-13137(2002).
CC -!- FUNCTION: Metalloproteinase inhibitor.
CC -!- SUBUNIT: Homodimer.
CC -!- TISSUE SPECIFICITY: Blood and milk.

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CC -1- PTM: N-glycosylated.
CC -1- MASS SPECTROMETRY: MW=42691; METHOD=WALDI; RANGE=1-291;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR011015; LEW-like.
DR Pfam: PF00047; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Metalloprotease inhibitor; Repeat.
FT DOMAIN 22 79
FT DOMAIN 114 171
FT DOMAIN 191 288
FT DISULFID 28 74
FT DISULFID 121 163
FT DISULFID 213 265
FT CARBOHYD 23 23
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 175 175
FT CARBOHYD 175 175
SQ SEQUENCE 291 AA; 32390 MW; 17A496227569A65B CRC64;

Query Match 100.0%; Score 69; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWI 12
DB 1 LKAMDPTPLWI 12

RESULT 3
QBHZ75 PRELIMINARY; PRT; 140 AA.
AC Q8HZ75;
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha 1B glycoprotein DVOP51-D (Fragment).
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
RP SEQUENCE FROM N.A.
RA Martinez M.E., Pierce J.R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY131000; AAN06911.1; -.
DR HSSP; O76036; 10LL.
DR InterPro: IPR007110; Ig-like.
FT NON_TER 1 1
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15297 MW; E19D071A76AA5A7F CRC64;

Query Match 87.0%; Score 60; DB 2; Length 140;
Best Local Similarity 91.7%; Pred. No. 0.072;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWI 12
DB 42 LKAMDPTPLWI 53

RESULT 4
QBHZ74 PRELIMINARY; PRT; 291 AA.
AC Q8HZ74;
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha 1B glycoprotein DVOP114 (Fragment).
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
RP SEQUENCE FROM N.A.
RA Martinez M.E., Pierce J.R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY131001; AAN06912.1; -.
DR HSSP; O8NHL6; 1GOX.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 291 291
SQ SEQUENCE 291 AA; 32509 MW; BEC282838A1C0BF4 CRC64;

Query Match 87.0%; Score 60; DB 2; Length 291;
Best Local Similarity 91.7%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWI 12
DB 1 LKAMDPTPLWI 12

RESULT 5
QBHYX5 PRELIMINARY; PRT; 314 AA.
AC Q8HYX5;
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Venom metalloproteinase inhibitor DM43b precursor.
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE FROM N.A.
RA Trugilho M.R.O., Junqueira-de-Azevedo I.L.M., Neves-Ferreira A.G.C.,
RA Domont G.B., Ho P.L., Perales J.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY163806; AAN64698.1; -.
DR HSSP; P24071; 1OVZ.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW SIGNAL.
FT CHAIN 1 23 Potential.
FT CHAIN 24 314 venom metalloproteinase inhibitor DM43b.
SQ SEQUENCE 314 AA; 34604 MW; 69D55F54486D35A5 CRC64;

Query Match 75.4%; Score 52; DB 2; Length 314;
Best Local Similarity 83.3%; Pred. No. 3.3;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWI 12
DB 24 LKAMDPTPLWI 35

RESULT 6
QB3ZB2 PRELIMINARY; PRT; 227 AA.
AC Q73ZB2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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DE Hypothetical protein.
OS OrderedLocusNames=MAP1691c;
GN Bacteriophage paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang Q., Anonin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017233; AAS04008.1; -
KW Complete proteome.
SQ SEQUENCE 227 AA; 24027 MW; 952EA4962C0BE199 CRC64;

Query Match 72.5%; Score 50; DB 2; Length 227;
Best Local Similarity 72.7%; Pred. No. 5;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPLW 11
|:|:|:|:|
DB 146 LAALDRPPLW 156

RESULT 7
QYQ848 PRELIMINARY; PRT; 370 AA.
AC QYQ848;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCP7225 (Fragment).
GN Name=agCG51396; ORFNames=ENSGG000000014288;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 2 C2 domains.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008848; EAA07048.1; -
DR HSSP; P21707; IKSW.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008021; C:synaptic vesicle; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002149; A:atropin_recept.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CaLB.
DR Pfam; PF00168; C2; 2.
DR PRINTS; PR00360; C2DOMAIN.
DR PROSITE; PS50004; C2_DOMAIN_2; 2.
FT NON_TER 1
SQ SEQUENCE 370 AA; 40989 MW; C558FDA3D5CD8D8F CRC64;

Query Match 66.7%; Score 46; DB 2; Length 370;
Best Local Similarity 54.5%; Pred. No. 37;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTPLW 11
|:|:|:|:|
DB 294 IRLDPTPIW 304

RESULT 8
QYQ833V1 PRELIMINARY; PRT; 128 AA.
ID Q833V1

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AC Q833V1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Conserved domain protein.
GN OrderedLocusNames=EF1825;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.N., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.N.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
DR EMBL; AE016952; AA081592.1; -
DR TIGR; EF1825; -
KW Complete proteome.
SQ SEQUENCE 128 AA; 14458 MW; 43459A9BE814572F CRC64;

Query Match 65.2%; Score 45; DB 2; Length 128;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPTPLW 12
|:|:|:|:|
DB 76 NPTPLW 83

RESULT 9
QYQJ7 PRELIMINARY; PRT; 467 AA.
ID QYQJ7;
AC QYQJ7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Organic anion transporter OATv1.
GN Name=OATv1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Apical membrane of renal proximal tubule in kidney cortex;
RX MEDLINE=22753825; PubMed=12740363; DOI=10.1074/jbc.M303210200;
RA Jutabha P., Kanai Y., Hosoyama M., Chairungdua A., Kim D.K.,
RA Iribe Y., Babu E., Kim J.Y., Anzai N., Chatsudhipong V., Endou H.;
RT "Identification of a novel voltage-driven organic anion transporter
RT present at apical membrane of renal proximal tubule.";
RL J. Biol. Chem. 278:27930-27938(2003).
DR EMBL; AB104465; BAC76761.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS50850; MFS; 1.
SQ SEQUENCE 467 AA; 52069 MW; 2B065005C3FDCAB6 CRC64;

Query Match 65.2%; Score 45; DB 2; Length 467;
Best Local Similarity 58.3%; Pred. No. 69;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPLW 12

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DR WormPep; C25B8.6; CE30877.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003707; F:steroid hormone receptor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000536; Hmon_recept_lig.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR000324; Vtcd_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR PRINTS; PR00350; VITAMINDR.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; ZNF_C4; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 477 AA; 54900 MW; 9D16A8FF3BDC0241 CRC64;

Query Match 63.8%; Score 44; DB 2; Length 477;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KAMDPTPLWI 12
Db 18 KLLHSPPMWI 28

RESULT 12
Y4VJ_RHISN STANDARD; PRT; 351 AA.
AC Q53218;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 05-JUL-2004 (Rel. 44; Last annotation update)
DE Hypothetical 39.2 kDa protein y4vJ.
GN ORFNames=y4vJ;
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
RN [2]
RP SEQUENCE OF 1-279 FROM N.A.
RX MEDLINE=96389014; PubMed=8796346;
RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RT NGR234 using dye terminators and a thermostable 'sequenase': a
RT beginning.";
RL Genome Res. 6:590-600(1996).
CC -!- SIMILARITY: Belongs to the bacterial luciferase oxidoreductase
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; Z68203; CA92425.1; -.
CC EMBL; AE000101; AAB91898.1; -.
CC InterPro; IPR002103; Bac_luciferase.
CC InterPro; IPR011251; Luciferase_like.

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DR Pfam; PF00296; Bac_luciferase; 1.
KW Hypothetical protein; Monooxygenase; Oxidoreductase; Plasmid.
SQ SEQUENCE 351 AA; 39158 MW; 866BDE3B8A40C88D CRC64;

Query Match 62.3%; Score 43; DB 1; Length 351;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PTPPLWI 12
Db 167 PTPPIWI 173

RESULT 13
Q8VM74 PRELIMINARY; PRT; 354 AA.
ID Q8VM74;
AC Q8VM74;
DT 01-MAR-2002 (TrEMBLrel. 20; Created)
DT 01-MAR-2002 (TrEMBLrel. 20; Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24; Last annotation update)
DE Putative LuxA.
OS Rhizobium sp. (strain BR816).
OG Plasmid pSymA.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=48291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR816;
RA Luyten E., Verreth C., Vanderleyden J.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BR816;
RA Luyten E., Swinnen E., Verreth C., Vlassak K., Dombrecht B.,
RA Vanderleyden J.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; U26451; AAL61964.1; -.
DR Pfam; PF00296; Bac_luciferase; 1.
KW Plasmid.
SQ SEQUENCE 354 AA; 39367 MW; 9D18A3F09BA70A42 CRC64;

Query Match 62.3%; Score 43; DB 2; Length 354;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PTPPLWI 12
Db 167 PTPPIWI 173

RESULT 14
Q846T8 PRELIMINARY; PRT; 360 AA.
ID Q846T8;
AC Q846T8;
DT 01-JUN-2003 (TrEMBLrel. 24; Created)
DT 01-JUN-2003 (TrEMBLrel. 24; Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25; Last annotation update)
DE Hypothetical adventurous gliding motility protein M.
GN Name=agmM;
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cythobacteriaceae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RA Hartzell P.L., Youderian P.A.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -!- COPACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SIMILARITY: Belongs to the peptidase M48 family.
DR EMBL; AY197568; AAO66299.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.

```

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001915; Peptidase_M48.
 DR Pfam; PF01435; Peptidase_M48; I.
 KW Hydrolase; Hypothetical protein; Metalloprotease; Protease; Zinc.
 SQ SEQUENCE 360 AA; 40304 MW; 98AB27E93EAC023 CRC64;

Query Match 62.3%; Score 43; DB 2; Length 360;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPLWI 12
 |||||:
 Db 332 MDPEPRWV 340

RESULT 15

Q9UZG1 PRELIMINARY; PRT; 695 AA.
 AC Q9UZG1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=PAB1590;
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GE5 / Orsay;
 RX MEDLINE=22511545; PubMed=12622808;
 RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
 RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
 RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
 RT "An integrated analysis of the genome of the hyperthermophilic
 RT archaeon Pyrococcus abyssi."
 RL Mol. Microbiol. 47:1495-1512(2003).
 DR EMBL; AJ248286; CAB50098.1; -.
 DR FIR; E75099; E75099.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 695 AA; 79999 MW; 371E0E402210F551 CRC64;

Query Match 62.3%; Score 43; DB 2; Length 695;
 Best Local Similarity 60.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTPLWI 12
 |||||:
 Db 561 ANDPEPPMWL 570

Search completed: May 26, 2005, 18:43:24
 Job time : 92.68 secs

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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:17:22 ; Search time 103.2 Seconds
(without alignments)
44.972 Million cell updates/sec

Title: US-10-047-945-4

Perfect score: 69

Sequence: 1 LKAMDPTPLWI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	12	7	ABB80225 Synthetic
2	69	100.0	15	2	AAW11575
3	69	100.0	15	2	AAW53841 N-terminu
4	69	100.0	15	7	ABB80223 Synthetic
5	65	94.2	11	7	ABB80226 Synthetic
6	54	78.3	10	2	AAW53843 N-terminu
7	54	78.3	10	7	ABB80222 Synthetic
8	50	72.5	9	7	ABB80227 Synthetic
9	45	65.2	137	7	ADH88053 Enterococ
10	44	63.8	156	4	ABG22890 Novel hum
11	44	63.8	303	4	ABG18144 Novel hum
12	43	62.3	393	4	ABB80228 Synthetic
13	43	62.3	932	8	ADM98800 HMG-CoA r
14	43	62.3	1189	2	AAW56496 TATA-bind
15	43	62.3	1213	2	AAW05086 Drosophil
16	43	62.3	1213	2	AAW25029 TATA-bind
17	43	62.3	1219	4	ABB62618 Drosophil
18	43	62.3	94	4	AAO02179 Human pol
19	42	60.9	242	7	ADB90591 Human pit
20	42	60.9	299	7	ADB90617 Human pit
21	42	60.9	612	8	ADH39800 Streptomy
22	42	60.9	1336	6	ABR47496 Breast ca
23	42	60.9	1336	8	ADP18673 Human pro
24	42	60.9	1457	4	AAU32796 Novel hum
25	42	60.9	1457	4	AAU32796 Novel hum

26	41	59.4	9	6	ABR12621 Human can
27	41	59.4	9	6	ABR12017 Human can
28	41	59.4	9	6	ABR12854 Human can
29	41	59.4	10	6	ABR12743 Human can
30	41	59.4	10	6	ABR11875 Human can
31	41	59.4	10	6	ABR12121 Human can
32	41	59.4	10	6	ABR12948 Human can
33	41	59.4	10	6	ABR12106 Human can
34	41	59.4	10	6	ABR12294 Human can
35	41	59.4	10	6	ABR12738 Human can
36	41	59.4	15	6	ABR33125 Human can
37	41	59.4	15	6	ABR33383 Human can
38	41	59.4	15	6	ABR33116 Human can
39	41	59.4	15	6	ABR33427 Human can
40	41	59.4	15	6	ABR33363 Human can
41	41	59.4	37	4	ABB42105 Peptide #
42	41	59.4	37	4	AAW75798 Human bon
43	41	59.4	37	4	AAW62985 Human bra
44	41	59.4	64	4	ABB40295 Peptide #
45	41	59.4	64	4	AAW33978 Peptide #

ALIGNMENTS

RESULT 1

ABB80225
ID ABB80225 standard; peptide; 12 AA.

XX AC ABB80225;

XX DT 06-NOV-2003 (first entry)

XX DB Synthetic LTNP, LT-12.

XX KW Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E; IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.

XX OS Synthetic.

XX WO2003060471-A2.

XX PD 24-JUL-2003.

XX PF 14-JAN-2003; 2003WO-US001044.

XX PR 14-JAN-2002; 2002US-00047945.

XX PA (LIPP/) LIPPS B V.

XX PA (LIPP/) LIPPS F W.

XX PI Lipps BV, Lipps FW;

XX WPI; 2003-636703/60.

XX DR Asaying a human endogenous protein (e.g. IGE, nerve growth factor,

XX PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.

XX PS Claim 7; Page 4; 24pp; English.

XX CC The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNP) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IGE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IGE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid

CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 XX
 XX Sequence 12 AA;

Query Match 100.0%; Score 69; DB 7; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00033; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0;

QY 1 LKAMDPTPLWI 12
 |||||
 Db 1 LKAMDPTPLWI 12

RESULT 2

AAW1575
 ID AAW1575 standard; peptide; 15 AA.

XX AC AAW1575;

XX DT 25-MAR-2003 (revised)
 XX DT 20-MAR-1997 (first entry)

XX DE N-terminal peptide from lethal toxin neutralising factor.

XX KW Lethal toxin neutralising factor; LTNP; opossum; bee toxin; snake bite.
 XX KW scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.

XX OS Didelphis virginiana.

XX PN US5576297-A.

XX PD 19-NOV-1996.

XX PF 22-SEP-1994; 94US-00310340.

XX PR 10-MAY-1993; 93US-00058387.

XX PA (LIPP/) LIPPS B V.
 XX PA (LIPP/) LIPPS F W.

XX PI Lipps FW, Lipps BV;

XX DR WPI; 1997-011287/01.

XX PT Treatment of victims of bee or scorpion stings or plant or bacterial
 XX PT toxins - by admin. of lethal toxin-neutralising factor or its N-terminal
 XX PT peptide.

XX PS Claim 7; Col 9; 9pp; English.

XX CC The present sequence is from the N-terminus of a 68 kD protein purified
 CC from the serum of the opossum *Didelphis virginiana*. The full-length
 CC protein is a lethal toxin neutralising factor (LTNP). The use of purified
 CC LTNP or of the chemically synthesised 15mer N-terminal peptide for
 CC treating victims of bee stings, scorpion stings and bacterial or plant
 CC toxins is claimed. The patent disclosure does not provide any evidence
 CC for neutralising activity against these various toxins. There is evidence
 CC of significant neutralising activity of the opossum LTNP and the 15mer
 CC peptide against venom from snakes of the families Crotalidae, Elapidae,
 CC Hydroliidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 69; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00041;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTPLWI 12
 |||||
 Db 1 LKAMDPTPLWI 12

RESULT 3

AAW53841
 ID AAW53841 standard; peptide; 15 AA.

XX AC AAW53841;

XX DT 08-JUL-1998 (first entry)

XX DE N-terminus of opossum LTNP.

XX KW LTNP; lethal toxin neutralising factor; opossum; envenomation; therapy;
 XX KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
 XX KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
 XX KW histamine reaction treatment.

XX OS Didelphis virginiana.

XX PN US5744449-A.

XX PD 28-APR-1998.

XX PF 03-JUN-1996; 96US-00657163.

XX PR 10-MAY-1993; 93US-00058387.

XX PR 22-SEP-1994; 94US-00310340.

XX PA (LIPP/) LIPPS B V.

XX PA (LIPP/) LIPPS F W.

XX PI Lipps FW, Lipps BV;

XX DR WPI; 1998-271108/24.

XX PT Lethal Toxin Neutralising Factor peptide from opossum - can neutralise

XX PT venom(s) from all major families of poisonous snakes.

XX PS Claim 1; Col 11; 11pp; English.

XX CC This sequence represents the peptide of the invention. It is a Lethal
 CC Toxin Neutralising Factor (LTNP) moiety from a 68 kDa anti-haemorrhagic
 CC protein derived from an opossum. The peptide can be used in a method for
 CC treating a victim of envenomation from a poisonous snake, preferably a
 CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
 CC is useful for the treatment of snake bites, sepsis, allergies caused by
 CC the environment and treatment of bee or scorpion stings or toxicities
 CC caused by plant or bacterial toxins. The peptide can also be used in
 CC histamine reaction treatment. The peptide can be used in envenomation
 CC treatment for a variety of snakes without prior identification of the
 CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 69; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00041;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWI 12
 |||||
 Db 1 LKAMDPTPLWI 12

RESULT 4

ABB80223

DE N-terminus of opossum LTNF.
 XX LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;
 KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
 KW histamine reaction treatment.
 XX
 XX Didelphis virginiana.
 OS
 XX US5744449-A.
 PN
 XX 28-APR-1998.
 PD
 XX
 XX 03-JUN-1996; 96US-00657163.
 PF
 XX 10-MAY-1993; 93US-00058387.
 PR
 XX 22-SEP-1994; 94US-00310340.
 PR
 XX (LIPPP/) LIPPS B V.
 PA
 XX (LIPPP/) LIPPS F W.
 PA
 XX Lipps FW, Lipps BV;
 PI
 XX WPI; 1998-271108/24.
 DR
 XX Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
 XX venom(s) from all major families of poisonous snakes.
 PT
 XX Claim 7; Col 11; lppp; English.
 PS
 XX This sequence represents the peptide of the invention. It is a Lethal
 CC Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic
 CC protein derived from an opossum. The peptide can be used in a method for
 CC treating a victim of envenomation from a poisonous snake, preferably a
 CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
 CC is useful for the treatment of snake bites, sepsis, allergies caused by
 CC the environment and treatment of bee or scorpion stings or toxicities
 CC caused by plant or bacterial toxins. The peptide can also be used in
 CC histamine reaction treatment. The peptide can be used in envenomation
 CC treatment for a variety of snakes without prior identification of the
 CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins
 CC
 XX Sequence 10 AA;
 SQ
 Query Match 78.3%; Score 54; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.067;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTPPL 10
 DB 1 LKAMDPTPPL 10
 RESULT 7
 ABB80222
 ID ABB80222 standard; peptide; 10 AA.
 XX
 XX ABB80222;
 AC
 XX 06-NOV-2003 (first entry)
 DT
 XX Synthetic LTNF, LT-10.
 DE
 XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 XX Synthetic.
 OS

XX WO2003060471-A2.
 PN
 XX 24-JUL-2003.
 PD
 XX 14-JAN-2003; 2003WO-US001044.
 PF
 XX 14-JAN-2002; 2002US-00047945.
 PR
 XX (LIPPP/) LIPPS B V.
 PA
 XX (LIPPP/) LIPPS F W.
 PA
 XX Lipps BV, Lipps FW;
 PI
 XX WPI; 2003-636703/60.
 DR
 XX Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 PT
 XX Claim 7; Page 3; 24pp; English.
 PS
 XX The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IgE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA
 CC
 XX Sequence 10 AA;
 SQ
 Query Match 78.3%; Score 54; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.067;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKAMDPTPPL 10
 DB 1 LKAMDPTPPL 10
 RESULT 8
 ABB80227
 ID ABB80227 standard; peptide; 9 AA.
 XX
 XX ABB80227;
 AC
 XX 06-NOV-2003 (first entry)
 DT
 XX Synthetic LTNF, LT-9.
 DE
 XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 XX Synthetic.
 OS
 XX WO2003060471-A2.
 PN
 XX

```

PD 24-JUL-2003.
XX
PF 14-JAN-2003; 2003WO-US001044.
XX
PR 14-JAN-2002; 2002US-00047945.
XX
PA (LIPP/) LIPPS B V.
PA (LIPP/) LIPPS F W.
XX
PI Lipps BV, Lipps FW;
XX
DR WPI; 2003-636703/60.
XX
XX
PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT asthma or diabetes, by employing an ELISA on a saliva sample from a
PT patient.
XX
PS Claim 7; Page 4; 24pp; English.
XX
CC The sequences given in ABB80222-28 represent lethal toxin neutralising
CC factor (LTNF) peptides which may be used for reducing elevated levels of
CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor
CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
CC particular, the methods of the invention are useful for diagnosing and
CC treating conditions with elevated serum IgE levels, e.g. asthma,
CC diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid
CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
CC the protein may be monitored by assaying a human endogenous protein by
CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
CC sample using an anti-serum that is specific for the protein. Saliva
CC collection is relatively non-invasive when compared to blood collection
CC for serum. Saliva can be centrifuged immediately, whereas blood requires
CC clotting time before centrifugation to separate serum. Saliva proteins
CC can be assayed by a simple ELISA test, whereas an assay of proteins from
CC serum requires a more complicated sandwich type ELISA
XX
XX Sequence 9 AA;
XX
Query Match 72.5%; Score 50; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 LKAMDPTPP 9
Db 1 LKAMDPTPP 9
XX
RESULT 9
ADH88053
ID ADH88053 standard; protein; 137 AA.
XX
AC ADH88053;
XX
XX 22-APR-2004 (first entry)
XX
DE Enterococcus faecalis polypeptide #2533.
XX
KW Enterococcus faecalis infection; transcription regulatory element;
KW antibacterial.
XX
OS Enterococcus faecalis.
XX
XX US6617156-B1.
XX
PD 09-SEP-2003.
XX
PF 13-AUG-1998; 98US-00134000.
XX
PR 15-AUG-1997; 97US-0055778P.
XX
PA (DOUC/) DOUCETTE-STAMM L A.
XX
PA (BUSH/) BUSH D.
XX
PI Doucette-Stamm LA, Bush D;
XX
DR WPI; 2003-895394/82.
DR N-PSDB; ADH84648.
XX
XX New nucleic acid comprising a sequence encoding an Enterococcus faecalis
XX polypeptide, useful for preparing a composition for diagnosing or
XX treating E. faecalis infection.
XX
PS Disclosure; SEQ ID NO 5938; 193pp; English.
XX
XX The invention relates to Enterococcus faecalis polynucleotides and
XX polypeptides. The invention also relates to a recombinant expression
XX vector comprising a polynucleotide operably linked to a transcription
XX regulatory element, a cell comprising a recombinant vector, a method for
XX producing an E. faecalis polypeptide, an isolated nucleic acid comprising
XX a sequence not given in the specification, a recombinant vector
XX comprising the nucleic acid and a cell comprising the recombinant vector.
XX The polynucleotides can be used to detect the presence of E. faecalis in
XX a sample. The sequences are useful for preparing a composition for
XX diagnosing or treating Enterococcus faecalis infection. This sequence
XX represents an E. faecalis polypeptide of the invention.
XX
SQ Sequence 137 AA;
XX
Query Match 65.2%; Score 45; DB 7; Length 137;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 5 DPTPPLW 12
Db 85 NPTPPLW 92
XX
RESULT 10
ABG22890
ID ABG22890 standard; protein; 156 AA.
XX
AC ABG22890;
XX
XX 18-FEB-2002 (first entry)
XX
DT Novel human diagnostic protein #22881.
XX
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
XX WO200175067-A2.
XX
PN 11-OCT-2001.
XX
PD 30-MAR-2001; 2001WO-US008631.
XX
PF 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
DR N-PSDB; AAS87077.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20; SEQ ID NO 53249; 103pp; English.

```

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 156 AA;
 Query Match 63.8%; Score 44; DB 4; Length 156;
 Best Local Similarity 54.5%; Pred. No. 40;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 KAMDPTPLWI 12
 || || ||:
 141 KAQPPAPPMWL 151
 DB
 RESULT 11
 ABG18144
 ID ABG18144 standard; protein; 303 AA.
 AC ABG18144;
 XX
 XX 18-FEB-2002 (first entry)
 DT
 DE Novel human diagnostic protein #18135.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 KW
 OS Homo sapiens.
 XX
 XX WO200175067-A2.
 PN
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US008631.
 PF
 XX 31-MAR-2000; 2000US-00540217.
 PR
 XX 23-AUG-2000; 2000US-00649167.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR
 XX N-PSDB; AAS82331.
 DR
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 PT
 XX Claim 20; SEQ ID NO 48503; 103pp; English.
 PS
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC

CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 303 AA;
 Query Match 63.8%; Score 44; DB 4; Length 303;
 Best Local Similarity 54.5%; Pred. No. 78;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 KAMDPTPLWI 12
 : || || ||:
 39 EASDFVPYVW 49
 DB
 RESULT 12
 ABB80228
 ID ABB80228 standard; peptide; 8 AA.
 XX
 AC ABB80228;
 XX
 XX 06-NOV-2003 (first entry)
 DT
 XX
 DE Synthetic LTNP, LT-8.
 XX
 XX Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.
 XX
 XX WO2003060471-A2.
 PN
 PD 24-JUL-2003.
 XX
 XX 14-JAN-2003; 2003WO-US001044.
 PF
 XX 14-JAN-2002; 2002US-00047945.
 PR
 XX (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.
 XX
 XX Lipps BV, Lipps FW;
 PI
 XX WPI; 2003-636703/60.
 DR
 XX Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a
 PT patient.
 PT
 XX Claim 7; Page 4; 24pp; English.
 PS
 XX

CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNP) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematous (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX
 SQ Sequence 8 AA;

Query Match 62.3%; Score 43; DB 7; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
 |||||
 Db 1 LKAMDPTP 8

RESULT 13
 AAM79784
 ID AAM79784 standard; protein; 393 AA.
 XX AC AAM79784;
 XX AC AAM79784;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human protein SEQ ID NO 3430.
 XX DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX OS Homo sapiens.
 XX OS WO200157190-A2.
 XX PN 09-AUG-2001.
 XX PD 05-FEB-2001; 2001WO-US004098.
 XX PF 03-FEB-2000; 2000US-00496914.
 XX PR 27-APR-2000; 2000US-00560875.
 XX PR 20-JUN-2000; 2000US-00598075.
 XX PR 19-JUL-2000; 2000US-00620325.
 XX PR 01-SEP-2000; 2000US-00654936.
 XX PR 15-SEP-2000; 2000US-00663561.
 XX PR 20-OCT-2000; 2000US-00693325.
 XX PR 30-NOV-2000; 2000US-00728422.
 XX PA (HYSE-) HYSEQ INC.
 XX PA Tang YT, Liu Q, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QN, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI; 2001-476283/51.
 DR N-PSDB; AAK52917.
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.

PS Claim 20; Page 332; 6221pp; English.
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication

XX
 SQ Sequence 393 AA;

Query Match 62.3%; Score 43; DB 4; Length 393;
 Best Local Similarity 54.5%; Pred. No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLW 11
 :||:||||
 Db 11 IKLSPLPLW 21

RESULT 14
 ADM98800
 ID ADM98800 standard; protein; 932 AA.
 XX AC ADM98800;
 XX DT 01-JUL-2004 (first entry)
 XX DE HMG-CoA reductase polypeptide #53.
 KW Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor;
 KW diterpene synthase; defence toxin; volatile defensive signal;
 KW pollinator attractant; photoprotectant; HMG-CoA reductase; enzyme.
 XX OS Strongylocentrotus purpuratus.
 XX OS US2004072323-A1.
 XX PN 15-APR-2004.
 XX PD 07-JAN-2002; 2002US-00041018.
 XX PF 05-JAN-2001; 2001US-0259880P.
 XX PR (MATS/) MATSUDA S P T.
 XX PA (HART/) HART E A.
 XX PA Matsuda SPT, Hart EA;
 XX WPI; 2004-373921/35.
 XX New unicellular organisms comprising exogenous nucleic acids encoding a
 PT geranylgeranyl pyrophosphate and a diterpene synthase, useful for
 PT producing diterpenes and diterpene precursors.
 XX Disclosure; SEQ ID NO 220; 38pp; English.
 XX The invention relates to a unicellular organism for producing a diterpene
 CC or diterpene precursor comprising an exogenous nucleic acid sequence
 CC encoding a geranylgeranyl pyrophosphate synthase under the control of a
 CC promoter operable in the organism, and an exogenous nucleic acid sequence
 CC encoding a diterpene synthase under the control of a promoter operable in
 CC the organism. The invention also relates to methods of producing a
 CC diterpene or diterpene precursor and a method of isolating a diterpene
 CC synthase comprising growing several cells in the presence of a
 CC polyaromatic resin to make a cell/resin mixture, where at least one of

CC the cells further comprises at least one isolated and purified nucleic
 CC acid sequence of a yeast expression library, and the expression of the
 CC nucleic acid sequence is regulated by an inducible promoter under
 CC conditions where the expression is induced, filtering the cell/resin
 CC mixture, extracting the cell/resin mixture with alcohol to produce an
 CC organic eluent and analysing the organic eluent by a screening method
 CC including chromatography and/or spectroscopy, to identify the nucleic
 CC acid sequence encoding the diterpene synthase. The unicellular
 CC microorganism is useful as a diterpene or diterpene precursor producing
 CC system. Diterpenes, in plants, serve as defence toxins, volatile
 CC defensive signals, pollinator attractants and photoprotectants. This
 CC sequence represents an HMGR-CoA reductase polypeptide used in the scope of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification but was obtained in electronic format from
 CC USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 932 AA;
 Query Match 62.3%; Score 43; DB 8; Length 932;
 Best Local Similarity 70.0%; Pred. No. 3 4e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMDPTPLPW 11
 Db 298 KKIDPTMPLW 307

RESULT 15

AARS6496
 ID AARS6496 standard; protein; 1189 AA.

XX AC AARS6496;

XX DT 25-MAR-2003 (revised)
 DT 23-MAR-1995 (first entry)

XX DE TATA-binding protein-associated factor dTAFI50.

XX KW TATA-binding protein associated factor; dTAFI50; screening; diagnostic;
 XX therapeutic; gene transcription regulation.

XX OS Drosophila.

XX FH Key Location/Qualifiers

FT Misc-difference 923 /note= "Val or Leu"

FT Misc-difference 1106

FT Misc-difference 1172 /note= "Arg, Pro or His"

FT Misc-difference 1176 /note= "STOP"

FT Misc-difference 1176 /note= "STOP"

XX PN WO9417087-A1.

XX PD 04-AUG-1994.

XX PF 28-JAN-1994; 94WO-US001114.

XX PR 28-JAN-1993; 93US-00013412.

XX PR 30-JUN-1993; 93US-00087119.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Tjian R, Comai L, Dynlact BD, Hoey T, Ruppert S, Tanese N;

XX PI Wang E, Weinzierl ROJ;

XX DR WPI: 1994-264019/32.

XX DR N-PSDB; AAQ70733.

XX PT TATA-binding protein associated protein factors - and corresponding
 PT nucleotide sequence and deriv. antibodies, useful in screening,
 PT diagnostics and therapeutics.

XX PS Disclosure; Page 156; 180pp; English.

XX CC The TATA-binding protein associated factor hTAFI50 (including specific
 CC antibodies and fusion products) are used in drug screening, diagnostics
 CC and therapeutics. They are used in the development of specific
 CC biochemical assays for screening compounds that agonise or antagonise
 CC selected transcription factors involved in regulating gene expression
 CC associated with human pathology. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX SQ Sequence 1189 AA;

Query Match 62.3%; Score 43; DB 2; Length 1189;

Best Local Similarity 66.7%; Pred. No. 4 4e+02;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKAMDPTPLPW 12

Db 589 LSAMDDSPVLWI 600

Search completed: May 26, 2005, 18:36:56
 Job time : 104.2 secs

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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:43:39 ; Search time 78.72 Seconds
(without alignments)
52.587 Million cell updates/sec

Title: US-10-047-945-4

Perfect score: 69

Sequence: 1 LKAMDPTPLWI 12

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/FCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	12	US-10-047-945-4	Sequence 4, Appli
2	69	100.0	15	US-10-047-945-2	Sequence 2, Appli
3	65	94.2	11	US-10-047-945-5	Sequence 5, Appli
4	54	78.3	10	US-10-047-945-1	Sequence 1, Appli
5	50	72.5	9	US-10-047-945-6	Sequence 6, Appli
6	44	63.8	106	US-10-424-599-255201	Sequence 255201,
7	44	63.8	124	US-10-424-599-151167	Sequence 151167,
8	44	63.8	144	US-10-424-599-205702	Sequence 205702,
9	43	62.3	8	US-10-047-945-7	Sequence 7, Appli
10	43	62.3	129	US-10-437-963-168841	Sequence 168841,
11	43	62.3	932	US-10-041-018-220	Sequence 220, App
12	42	60.9	82	US-10-437-963-128480	Sequence 128480,
13	42	60.9	1336	US-10-177-293-228	Sequence 228, App

14	41	59.4	37	9	US-09-864-761-45321	Sequence 45321, A
15	41	59.4	41	15	US-10-424-599-173148	Sequence 173148,
16	41	59.4	64	9	US-09-864-761-39999	Sequence 39999, A
17	41	59.4	80	15	US-10-424-599-253125	Sequence 253125,
18	41	59.4	86	15	US-10-424-599-220724	Sequence 220724,
19	41	59.4	87	15	US-10-424-599-179202	Sequence 179202,
20	41	59.4	148	16	US-10-437-963-133945	Sequence 133945,
21	41	59.4	176	14	US-10-097-065-274	Sequence 274, App
22	41	59.4	176	15	US-10-372-876-274	Sequence 274, App
23	41	59.4	212	9	US-09-989-722-387	Sequence 387, App
24	41	59.4	212	9	US-09-989-723-387	Sequence 387, App
25	41	59.4	212	9	US-09-989-279-387	Sequence 387, App
26	41	59.4	212	9	US-09-989-727-387	Sequence 387, App
27	41	59.4	212	9	US-09-989-731-387	Sequence 387, App
28	41	59.4	212	9	US-09-989-732-387	Sequence 387, App
29	41	59.4	212	9	US-09-989-733-387	Sequence 387, App
30	41	59.4	212	9	US-09-991-073-387	Sequence 387, App
31	41	59.4	212	9	US-09-990-442-387	Sequence 387, App
32	41	59.4	212	9	US-09-991-163-387	Sequence 387, App
33	41	59.4	212	9	US-09-993-604-387	Sequence 387, App
34	41	59.4	212	9	US-09-990-456-387	Sequence 387, App
35	41	59.4	212	9	US-09-989-721-387	Sequence 387, App
36	41	59.4	212	9	US-09-992-598-387	Sequence 387, App
37	41	59.4	212	9	US-09-989-293A-387	Sequence 387, App
38	41	59.4	212	9	US-09-989-735-387	Sequence 387, App
39	41	59.4	212	9	US-09-990-444-387	Sequence 387, App
40	41	59.4	212	9	US-09-991-181-387	Sequence 387, App
41	41	59.4	212	9	US-09-989-730-387	Sequence 387, App
42	41	59.4	212	9	US-09-990-436-387	Sequence 387, App
43	41	59.4	212	9	US-09-993-687-387	Sequence 387, App
44	41	59.4	212	10	US-09-989-734-387	Sequence 387, App
45	41	59.4	212	10	US-09-997-653-387	Sequence 387, App
			212	10	US-09-989-724-387	Sequence 387, App

ALIGNMENTS

RESULT 1
US-10-047-945-4
; Sequence 4, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.
US-10-047-945-4

Query Match 100.0%; Score 69; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. NO. 0.00098;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LKAMDPTPLWI 12
Db 1 LKAMDPTPLWI 12

RESULT 2

US-10-047-945-2
; Sequence 2, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:

; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.

SERUM

US-10-047-945-2
Query Match 100.0%; Score 69; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWI 12
|||||
DB 1 LKAMDPTPLWI 12

RESULT 3

US-10-047-945-5
; Sequence 5, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:

; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.

US-10-047-945-5
Query Match 94.2%; Score 65; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLW 11
|||||
DB 1 LKAMDPTPLW 11

RESULT 4

US-10-047-945-1
; Sequence 1, Application US/10047945

; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.

; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.

SERUM

US-10-047-945-1
Query Match 78.3%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPL 10
|||||
DB 1 LKAMDPTPL 10

RESULT 5

US-10-047-945-6
; Sequence 6, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:

; APPLICANT: LIPPS, BINIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.

US-10-047-945-6
Query Match 72.5%; Score 50; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPP 9
|||||
DB 1 LKAMDPTPP 9

RESULT 6

US-10-424-599-255201
; Sequence 255201, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

```
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 255201
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_72469C.1.pep
US-10-424-599-255201

Query Match      63.8%; Score 44; DB 15; Length 106;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      6 PTPPLWI 12
Db      92 PTPPLWV 98

RESULT 7
US-10-424-599-151167
; Sequence 151167, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 151167
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_107527C.1.pep
US-10-424-599-151167

Query Match      63.8%; Score 44; DB 15; Length 124;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      5 DTPPLWI 12
Db      96 DPPLWV 103

RESULT 8
US-10-424-599-205702
; Sequence 205702, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
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; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 205702
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(144)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_27777C.1.pep
US-10-424-599-205702

Query Match      63.8%; Score 44; DB 15; Length 144;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      6 PTPPLWI 12
Db      28 PTPPLWV 34

RESULT 9
US-10-047-945-7
; Sequence 7, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (IGE)IMPLICATED DISORDERS
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
US-10-047-945-7

Query Match      62.3%; Score 43; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LKAMDPTP 8
Db      1 LKAMDPTP 8

RESULT 10
US-10-437-963-168841
; Sequence 168841, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
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;
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 168841
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67316C.1.pbp
US-10-437-963-168841

Query Match 62.3%; Score 43; DB 16; Length 129;
Best Local Similarity 63.6%; Pred. No. 71;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKAMDPTPLW 11
DB 84 LARMPSPPLW 94

RESULT 11
US-10-041-018-220
; Sequence 220, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 220
; LENGTH: 932
; TYPE: PRT
; ORGANISM: Strongylocentrotus purpuratus
US-10-041-018-220

Query Match 62.3%; Score 43; DB 15; Length 932;
Best Local Similarity 70.0%; Pred. No. 4.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMDPTPLW 11
DB 298 KKIDPTPLW 307

RESULT 12
US-10-437-963-128480
; Sequence 128480, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128480
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Oryza sativa

;
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30829C.1.pbp
US-10-437-963-128480

Query Match 60.9%; Score 42; DB 16; Length 82;
Best Local Similarity 75.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPLWI 12
DB 75 EPTPCWI 82

RESULT 13
US-10-177-293-228
; Sequence 228, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 228
; LENGTH: 1336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-228

Query Match 60.9%; Score 42; DB 14; Length 1336;
Best Local Similarity 77.8%; Pred. No. 9e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPLWI 12
DB 34 MDQPELWI 42

RESULT 14
US-09-864-761-45321
; Sequence 45321, Application US/09864761

Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aomicca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45321
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL133458.11
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68
; OTHER INFORMATION: SWISSPROT HIT: O53951, EVALUATE 6.40e+00
; OTHER INFORMATION: EST_HUMAN HIT: A1986481.1, EVALUATE 6.00e-16
US-09-864-761-45321

Query Match 59.4%; Score 41; DB 9; Length 37;
Best Local Similarity 54.5%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Cyt 2 KAMDPTPLWI 12
|:|:|:|:
Db 5 KSMGPAPPRWM 15

RESULT 15

US-10-424-599-173148

; Sequence 173148, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 173148
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_127369C.1.pap
US-10-424-599-173148

Query Match 59.4%; Score 41; DB 15; Length 41;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Cyt 5 DPTPLW 11
|:|:|:|:
Db 14 DPTPLW 20

Search completed: May 26, 2005, 19:17:48
Job time : 91.72 secs

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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:29:58 ; Search time 27.36 Seconds
(without alignments)
32.741 Million cell updates/sec

Title: US-10-047-945-4

Perfect score: 69

Sequence: 1 LKANDPTPLWI 12

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	15	1	US-08-310-340A-1
2	69	100.0	15	1	US-08-657-163A-1
3	54	78.3	10	1	US-08-657-163A-2
4	45	65.2	137	4	US-09-134-000C-5938
5	43	62.3	397	4	US-09-902-540-13316
6	43	62.3	1213	1	US-08-188-582-20
7	43	62.3	1213	1	US-08-646-715-20
8	41	59.4	253	4	US-09-270-767-43223
9	40	58.0	198	4	US-09-270-767-57545
10	40	58.0	360	4	US-09-270-767-42265
11	39	56.5	72	4	US-09-949-016-8760
12	39	56.5	206	2	US-08-477-396A-18
13	39	56.5	210	4	US-09-270-767-45215
14	38	55.1	267	2	US-07-857-224B-42
15	38	55.1	557	4	US-09-902-540-16548
16	38	55.1	1740	4	US-09-377-285B-40
17	37	53.6	15	3	US-08-602-999A-444
18	37	53.6	15	4	US-09-500-124-444
19	37	53.6	78	4	US-09-248-796A-21988
20	37	53.6	87	4	US-09-270-767-41296
21	37	53.6	87	4	US-09-270-767-56512
22	37	53.6	196	4	US-09-252-991A-26963
23	37	53.6	207	4	US-09-328-352-6054
24	37	53.6	210	4	US-09-071-035-232
25	37	53.6	256	4	US-09-071-035-230
26	37	53.6	265	4	US-09-270-767-43480
27	37	53.6	291	4	US-09-134-000C-6676

28	37	53.6	306	4	US-09-134-000C-6583	Sequence 6583, Ap
29	37	53.6	387	4	US-09-252-991A-30473	Sequence 30473, A
30	37	53.6	427	4	US-08-311-731A-216	Sequence 216, App
31	37	53.6	502	4	US-09-540-236-3413	Sequence 3413, App
32	37	53.6	528	4	US-09-270-767-42895	Sequence 42895, A
33	37	53.6	3170	2	US-07-642-734C-5	Sequence 5, Appli
34	37	53.6	3170	3	US-08-439-009A-5	Sequence 5, Appli
35	37	53.6	4928	3	US-09-036-987A-5	Sequence 5, Appli
36	37	53.6	4928	3	US-09-370-700-5	Sequence 5, Appli
37	37	53.6	4928	4	US-09-603-207-5	Sequence 5, Appli
38	36	52.2	119	4	US-09-248-796A-25521	Sequence 25521, A
39	36	52.2	200	4	US-09-252-991A-27890	Sequence 27890, A
40	36	52.2	230	3	US-09-187-789-7	Sequence 7, Appli
41	36	52.2	230	4	US-09-989-903-7	Sequence 7, Appli
42	36	52.2	259	4	US-09-949-016-10617	Sequence 10617, A
43	36	52.2	280	3	US-09-247-155-178	Sequence 178, App
44	36	52.2	323	4	US-09-489-039A-13655	Sequence 13655, A
45	36	52.2	338	4	US-09-248-796A-15934	Sequence 15934, A

ALIGNMENTS

RESULT 1

US-08-310-340A-1

; Sequence 1, Application US/08310340A

; Patent No. 5576297

; GENERAL INFORMATION:

; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS

; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND

; TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BINIE V. LIPPS

; STREET: 4509 MIMOSA DR.

; CITY: BELLAIRE

; STATE: TEXAS

; COUNTRY: USA

; ZIP: 77401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB

; COMPUTER: IBM COMPATIBLE

; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1

; SOFTWARE: MS WORD 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/310,340A

; FILING DATE: 22 SEPTEMBER 1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/058, 387

; FILING DATE: 10 MAY 1993

; ATTORNEY/AGENT INFORMATION:

; NAME:

; REGISTRATION NUMBER:

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 713-723-6845

; TELEFAX: 713-663-7290

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15

; TYPE: AMINO ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N

; ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:

; ORGANISM: DIDELPHIS VIRGINIANA

; STRAIN: WILD

INDIVIDUAL ISOLATE: TEXAS WILD
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDEPLHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXICOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
VOLUME: SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
US-08-310-340A-1

Query Match 100.0%; Score 69; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWI 12
DB 1 LKAMDPTPLWI 12

RESULT 2

US-08-657-163A-1
Sequence 1, Application US/08657163A
Patent No. 5744449

GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LTNFS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
TELEX:
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:
ORGANISM: DIDEPLHIS VIRGINIANA
STRAIN: WILD
INDIVIDUAL ISOLATE: TEXAS WILD
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
CLONE:
PUBLICATION INFORMATION:
AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDEPLHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXICOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
US-08-657-163A-1

Query Match 100.0%; Score 69; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWI 12
DB 1 LKAMDPTPLWI 12

RESULT 3

US-08-657-163A-2
Sequence 2, Application US/08657163A
Patent No. 5744449
GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LTNFS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 1:

;; APPLICATION NUMBER: 08/058,387
;; FILING DATE: 10 MAY 1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: JOHN R. CASPERSON
;; REGISTRATION NUMBER: 28,198
;; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 713-482-2961
;; TELEFAX: 713-663-7290
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10
;; TYPE: AMINO ACID
;; STRANDEDNESS: SINGLE
;; TOPOLOGY: LINEAR
;; MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N
;; ORIGINAL SOURCE: SYNTHETIC
;; US-08-657-163A-2

Query Match 78.3%; Score 54; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPL 10
Db 1 LKAMDPTPL 10

RESULT 4

;; US-09-134-000C-5938
;; Sequence 5938, Application US/09134000C
;; Patent No. 6617156
;; GENERAL INFORMATION:
;; APPLICANT: Lynn Doucette-Stamm et al
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;; FILE REFERENCE: 032796-032
;; CURRENT APPLICATION NUMBER: US/09/134,000C
;; PRIOR FILING DATE: 1998-08-13
;; PRIOR FILING DATE: 1997-08-15
;; NUMBER OF SEQ ID NOS: 6812
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 5938
;; LENGTH: 137
;; TYPE: PRT
;; ORGANISM: Enterococcus faecalis
;; US-09-134-000C-5938

Query Match 65.2%; Score 45; DB 4; Length 137;
Best Local Similarity 75.0%; Pred. No. 5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DPTPLWI 12
Db 85 NPTPLW 92

RESULT 5

;; US-09-902-540-13316
;; Sequence 13316, Application US/09902540
;; Patent No. 6833447
;; GENERAL INFORMATION:
;; APPLICANT: Goldman, Barry S.
;; APPLICANT: Hinkle, Gregory J.
;; APPLICANT: Slater, Steven C.
;; APPLICANT: Wiegand, Roger C.
;; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;; FILE REFERENCE: 38-10(15849)B

;; CURRENT APPLICATION NUMBER: US/09/902,540
;; CURRENT FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: 60/217,883
;; PRIOR FILING DATE: 2000-07-10
;; NUMBER OF SEQ ID NOS: 16825
;; SEQ ID NO 13316
;; LENGTH: 397
;; TYPE: PRT
;; ORGANISM: Myxococcus xanthus
;; US-09-902-540-13316

Query Match 62.3%; Score 43; DB 4; Length 397;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MDPTPLWI 12
Db 369 MDPEPRWV 377

RESULT 6

;; US-08-188-582-20
;; Sequence 20, Application US/08188582
;; Patent No. 5534410
;; GENERAL INFORMATION:
;; APPLICANT: Tjian, Robert
;; APPLICANT: Comai, Lucio
;; APPLICANT: Dynlacht, Brian D.
;; APPLICANT: Hoey, Timothy
;; APPLICANT: Ruppert, siegfried
;; APPLICANT: Tanese, Naoko
;; APPLICANT: Wang, Edith
;; APPLICANT: Weinzierl, Robert O.J.
;; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
;; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
;; NUMBER OF SEQUENCES: 36
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
;; STREET: 4 Embarcadero Center, Suite 3400
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-4187
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/188,582
;; FILING DATE: 28-JAN-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Osman, Richard A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 781-1989
;; TELEFAX: (415) 398-3249
;; TELEX: 910 277299
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1213 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-188-582-20

Query Match 62.3%; Score 43; DB 1; Length 1213;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWI 12

Db 620 LSAMDDSPVLWI 631

RESULT 7

US-08-646-715-20
; Sequence 20, Application US/08646715
; Patent No. 5637686
; GENERAL INFORMATION:
; APPLICANT: Tjian, Robert
; APPLICANT: Comai, Lucio
; APPLICANT: Dynlacht, Brian D.
; APPLICANT: Hoey, Timothy
; APPLICANT: Ruppert, Siegfried
; APPLICANT: Tanese, Naoko
; APPLICANT: Wang, Edith
; APPLICANT: Weinzierl, Robert O.J.
; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLHRH, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,715
; FILING DATE: 09-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/188,582
; FILING DATE: 28-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1213 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-646-715-20

Query Match 62.3%; Score 43; DB 1; Length 1213;
Best Local Similarity 66.7%; Pred. No. 11e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLWI 12
Db 620 LSAMDDSPVLWI 631

RESULT 8

US-09-270-767-43223
; Sequence 43223, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43223
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43223

Query Match 59.4%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDPTPL 10
Db 43 MDPTPL 49

RESULT 9

US-09-270-767-57545
; Sequence 57545, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57545
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57545

Query Match 58.0%; Score 40; DB 4; Length 198;
Best Local Similarity 54.5%; Pred. No. 48;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLW 11
Db 70 IKAVSPSNLW 80

RESULT 10

US-09-270-767-42265
; Sequence 42265, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42265
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42265

Query Match 58.0%; Score 40; DB 4; Length 360;
Best Local Similarity 54.5%; Pred. No. 91;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDPTPLW 11
Db 70 IKAVSPSPNLW 80

RESULT 11
US-09-949-016-8760
; Sequence 8760, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8760
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8760

Query Match 56.5%; Score 39; DB 4; Length 72;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTTP 9
Db 61 RTMDPTTP 68

RESULT 12
US-08-477-396A-18
; Sequence 18, Application US/08477396A
; Patent No. 5872235
; GENERAL INFORMATION:
; APPLICANT: Chen, Ian Bo
; APPLICANT: Bao, Shideng
; APPLICANT: Liu, Yuan
; TITLE OF INVENTION: A NOVEL TUMOR MARKER AND NOVEL METHOD OF
; ISOLATING SAME
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,396A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,488
; FILING DATE: 29-OCT-1993
; APPLICATION NUMBER: US 08/448,388
; FILING DATE: 28-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12502

; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DFCI-333BX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-477-396A-18

Query Match 56.5%; Score 39; DB 2; Length 206;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MDPTPLW 12
Db 82 LDGNPPLW 90

RESULT 13
US-09-270-767-45215
; Sequence 45215, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45215
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45215

Query Match 56.5%; Score 39; DB 4; Length 210;
Best Local Similarity 60.0%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KAMDPTPLW 11
Db 134 KSDDPTNPIW 143

RESULT 14
US-07-857-224B-42
; Sequence 42, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 267
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
FEATURE: Protein kinase; Table 8 Column 48
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-52
DATE: 1988
US-07-857-224B-42

Search completed: May 26, 2005, 19:08:40
Job time : 28.56 secs

Query Match 55.1%; Score 38; DB 2; Length 267;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPEL 10
Db 31 LKVDPTPEL 40

RESULT 15
US-09-902-540-16548
; Sequence 16548, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16548
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16548

Query Match 55.1%; Score 38; DB 4; Length 557;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTPLWI 12
Db 135 EPTPHWL 142

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:26:23 ; Search time 12.64 Seconds
(without alignments)
60.897 Million cell updates/sec

Title: US-10-047-945-7

Perfect score: 43

Sequence: 1 LKAMDPTP 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	88.4	792	2 T29187	hypothetical prote
2	35	81.4	237	2 A42013	alpha-1-B-glycopro
3	35	81.4	323	1 TWVVF6	protein kinase [EC
4	35	81.4	380	1 TVFVMM	protein kinase [EC
5	35	81.4	602	1 TVRTRR	protein kinase [EC
6	35	81.4	647	1 S00644	protein kinase raf
7	35	81.4	648	1 TVHUF6	protein kinase raf
8	35	81.4	648	1 TVRTRF	protein kinase raf
9	34	79.1	99	2 G64225	ribosomal protein
10	33	76.7	350	2 E87327	hypothetical prote
11	33	76.7	444	2 PD0001	protein-glutamine
12	33	76.7	638	1 TVXLRF	protein kinase raf
13	33	76.7	691	1 A29996	protein-glutamine
14	33	76.7	2717	2 A4203	DNA-binding protei
15	32	74.4	262	2 E64679	tryptophan synthas
16	32	74.4	408	2 A83370	probable transport
17	32	74.4	416	2 AF2070	hypothetical prote
18	32	74.4	548	2 A44302	protein-glutamine
19	32	74.4	620	2 AG1598	internalin like pr
20	32	74.4	638	2 I40725	2-isopropylmalate
21	32	74.4	680	2 JC5133	protein-glutamine
22	32	74.4	687	1 B39045	protein-glutamine
23	32	74.4	687	1 A39045	protein-glutamine
24	32	74.4	687	1 S19680	protein-glutamine
25	32	74.4	698	1 A47203	protein-glutamine
26	32	74.4	771	2 B38252	granulocyte colony
27	32	74.4	783	2 JH0329	granulocyte colony
28	32	74.4	863	2 C38252	granulocyte colony
29	31	72.1	142	2 AE1681	similar o transcri

30	31	72.1	180	2 T16668	hypothetical prote
31	31	72.1	253	2 T37152	probable oxidoredu
32	31	72.1	276	2 JC5285	carbonyl reductase
33	31	72.1	277	2 JC5284	carbonyl reductase
34	31	72.1	285	2 JC6206	catechol 1,2-dioxy
35	31	72.1	323	2 T21569	hypothetical prote
36	31	72.1	339	2 T36869	probable glycohyd
37	31	72.1	339	2 T49597	hypothetical prote
38	31	72.1	345	2 S21094	alpha-2-HS-glycopr
39	31	72.1	348	2 JC5431	countertryptin proc
40	31	72.1	361	2 G87706	hypothetical prote
41	31	72.1	375	2 A32827	fetuin precursor -
42	31	72.1	376	2 C84769	probable fibrillin
43	31	72.1	398	2 A81717	conserved hypotet
44	31	72.1	431	2 T33287	hypothetical prote
45	31	72.1	464	2 T17332	hypothetical prote

ALIGNMENTS

RESULT 1

T29187

hypothetical protein C55C3.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T29187

R;Wossnes, J.; Stellyes, L.

submitted to the EMBL Data Library, April 1996

A;Description: The sequence of C. elegans cosmid C55C3.

A;Reference number: Z20585

A;Accession: T29187

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-792 <WQE>

A;Cross-references: EMBL:U53335; PIDN:AAA96170.1; GSPDB:GN000022; CESP:C55C3.3

A;Experimental source: strain Bristol N2; clone C55C3

C;Genetics:

A;Gene: CESP:C55C3.3

A;Map position: 4

A;Introns: 17/1; 46/3; 139/2; 173/1; 204/3; 250/3; 266/3; 286/2; 327/1; 362/3; 393/3; 43

Query Match 88.4%; Score 38; DB 2; Length 792;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8

||| ||| |||

Db 133 LKAMDPTP 140

RESULT 2

A42013

alpha-1-B-glycoprotein - North American opossum (fragments)

C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)

C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004

C;Accession: A42013

R;Catanesse, J.J.; Kress, L.F.

Biochemistry 31, 410-418, 1992

A;Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hum

A;Reference number: A42013; MUID:92118834; PMID:1731898

A;Accession: A42013

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-237 <CAT>

A;Cross-references: UNIPROT:Q28359; GB:J05356

C;Keywords: glycoprotein

Query Match 81.4%; Score 35; DB 2; Length 237;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8

```

Db      1 LKAMDTP 8
|||||
RESULT 3
TVNMF6
protein kinase (EC 2.7.1.37) raf - murine sarcoma virus 3611
N/Alternate names: kinase-related transforming protein raf; raf proto-oncogene protein-e
C/Species: murine sarcoma virus 3611
A/Note: host Mus musculus (mouse)
C/Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C/Accession: A00638; A38020
R/Kan, N.C.; Flordellis, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.
Science 223, 813-816, 1984
A/Title: A common onc gene sequence transduced by avian carcinoma virus MH2 and by murin
A/Reference number: A00638; MUID:84121298; PMID:6320371
A/Accession: A00638
A/Molecule type: DNA
A/Residues: 1-323 <KAN>
A/Cross-references: UNIPROT:P00532
A/Experimental source: ATCC 45010
R/Mark, G.E.; Rapp, U.R.
Science 224, 285-289, 1984
A/Title: Primary structure of v-raf: relatedness to the src family of oncogenes.
A/Reference number: A38020; MUID:84172180; PMID:6324342
A/Accession: A38020
A/Molecule type: DNA
A/Residues: 1-323 <MAR>
C/Comment: This protein is translated as a gag-raf polypeptide.
C/Genetics:
A/Gene: raf
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: ATP; oncogene; phosphotransferase; serine/threonine-specific protein kinase;
F/22-288/Domain: protein kinase homology <KIN>
F/30-38/Region: protein kinase ATP-binding motif
F/50/Active site: Lys #status predicted

Query Match      81.4%; Score 35; DB 1; Length 323;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKAMDTP 8
|||
Db      52 LKVDPTP 59
|||||

RESULT 4
TVFVVM
protein kinase (EC 2.7.1.37) mil - avian myelocytomatosis virus MH2
N/Alternate names: kinase-related transforming protein mil (mht); mil proto-oncogene pro
C/Species: avian myelocytomatosis virus MH2
A/Note: host Gallus gallus (chicken)
C/Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C/Accession: A00639; B00638; A21137
R/Sutrave, P.; Bonner, T.I.; Rapp, U.R.; Jansen, H.W.; Patschinsky, T.; Bister, K.
Nature 309, 85-88, 1984
A/Title: Nucleotide sequence of avian retroviral oncogene v-mil: homologue of murine ret
A/Reference number: A00639; MUID:84191511; PMID:6325930
A/Accession: A00639
A/Molecule type: DNA
A/Residues: 1-380 <SUT>
A/Cross-references: UNIPROT:P00531; GB:K02082
A/Note: the authors translated the codon CAG for residue 58 as Gly
R/Kan, N.C.; Flordellis, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.
Science 223, 813-816, 1984
A/Title: A common onc gene sequence transduced by avian carcinoma virus MH2 and by murin
A/Reference number: A00638; MUID:84121298; PMID:6320371
A/Accession: B00638
A/Molecule type: DNA
A/Residues: 1-210,'E',212-380 <KAN>
A/Cross-references: GB:K02084
R/Kan, N.C.; Flordellis, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.
Proc. Natl. Acad. Sci. U.S.A. 81, 3000-3004, 1984

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A/Title: Nucleotide sequence of avian carcinoma virus MH2: two potential onc genes, one
A/Reference number: A21137; MUID:84221892; PMID:6328485
A/Accession: A21137
A/Molecule type: DNA
A/Residues: 1-210,'E',212-230,'E',232-380 <KA2>
A/Cross-references: GB:K02082
C/Comment: This protein is translated as a gag-mht or gag-mil polypeptide.
C/Genetics:
A/Gene: mht; mil
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: ATP; oncogene; phosphotransferase; polyprotein; serine/threonine-specific p;
F/80-346/Domain: protein kinase homology <KIN>
F/88-96/Region: protein kinase ATP-binding motif
F/108/Active site: Lys #status predicted

Query Match      81.4%; Score 35; DB 1; Length 380;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKAMDTP 8
|||
Db      110 LKVDPTP 117
|||||

RESULT 5
TVTRTR
protein kinase (EC 2.7.1.37) raf - rat
N/Alternate names: kinase-related transforming protein raf; raf proto-oncogene protein-r
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
C/Accession: B26126
R/Ishikawa, F.; Takaku, F.; Nagao, M.; Sugimura, T.
Mol. Cell. Biol. 7, 1226-1232, 1987
A/Title: Rat c-raf oncogene activation by a rearrangement that produces a fused protein.
A/Reference number: A26126; MUID:87172791; PMID:3550433
A/Accession: B26126
A/Molecule type: mRNA
A/Residues: 1-602 <ISH>
A/Cross-references: GB:M15428; NID:g206546; PIDN:AAA42002.1; PID:g206547
C/Genetics:
A/Gene: raf
C/Superfamily: rat protein kinase raf; protein kinase homology
C/Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonin
F/301-567/Domain: protein kinase homology <KIN>
F/309-317/Region: protein kinase ATP-binding motif
F/329/Active site: Lys #status predicted
F/453/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict

Query Match      81.4%; Score 35; DB 1; Length 602;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKAMDTP 8
|||
Db      331 LKVDPTP 338
|||||

RESULT 6
S00644
protein kinase raf-1 (EC 2.7.1.-) - chicken
N/Alternate names: kinase-related transforming protein raf-1; mht/raf; protein kinase c-
C/Species: Gallus gallus (chicken)
C/Date: 18-Oct-1989 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C/Accession: S00644; I50380; I50381
R/Koenen, M.; Sippl, A.E.; Trachmann, C.; Bister, K.
Oncogene 2, 179-185, 1988
A/Title: Primary structure of the chicken c-mil protein: identification of domains shar
A/Reference number: S00644; MUID:88217299; PMID:3285296
A/Accession: S00644
A/Molecule type: mRNA
A/Residues: 1-647 <KOE>
A/Cross-references: UNIPROT:P05625; EMBL:X07017; NID:G63232; PIDN:CAA30069.1; PID:G63233
R/Flordellis, C.S.; Kan, N.C.; Lautenberger, J.A.; Samuel, K.P.; Garon, C.F.; Papas, T.

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Virology 141, 267-274, 1985
A:Title: Analysis of the cellular proto-oncogene mht/raf: Relationship to the 5' sequence
A:Reference number: I50380; MUID:86098644; PMID:3002017
A:Accession: I50380
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 230-330 <FLO>
A:Cross-references: GB:K03048; NID:g212306; PIDN:AAA48951.1; PID:g212308
R:Jansen, H.W.; Bister, K.
Virology 143, 359-367, 1985
A:Title: Nucleotide sequence analysis of the chicken gene c-mil, the progenitor of the
A:Reference number: I50381; MUID:86045899; PMID:2998016
A:Accession: I50381
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 228-548, 'F', 550-647 <JAN>
A:Cross-references: GB:K03269; NID:g212319; PIDN:AAA48952.1; PID:g212321
C:Genetics:
A:Note: the list of introns may be incomplete
A:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A:Pathway: MAP kinase cascade
A:Note: after phosphorylation and activation by protein kinase C, phosphorylates and act
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:139-184/Domain: protein kinase C zinc-binding repeat homology <KZN>
F:347-613/Region: protein kinase ATP-binding motif
F:355-363/Domain: protein kinase ATP-binding motif
F:43.621/Binding site: phosphate (Ser) (covalent) #status predicted
F:139,165,168,184/Binding site: zinc (His, Cys, Cys) #status predicted
F:152,155,173,176/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:259/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:268/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted
F:375,393,468,470/Active site: Lys, Glu, Asp, Lys #status predicted
F:499/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 81.4%; Score 35; DB 1; Length 647;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
|||:||||
Db 377 LKVDPTP 384

RESULT 7
TVTRF6
Protein kinase raf-1 (EC 2.7.1.1) - human
N:Alternate names: kinase-related transforming protein raf-1; raf-1 proto-oncogene prote
N:Contains: protein kinase (EC 2.7.1.37)
C:Species: Homo sapiens (man)
C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C:Accession: A00637; I57580
R:Bonner, T.I.; Oppermann, H.; Seeburg, P.; Kerby, S.B.; Gunnell, M.A.; Young, A.C.; Rap
Nucleic Acids Res. 14, 1009-1015, 1986
A:Title: The complete coding sequence of the human raf oncogene and the corresponding st
A:Reference number: A00637; MUID:86120351; PMID:3003687
A:Accession: A00637
A:Molecule type: mRNA
A:Residues: 1-648 <BONI>
A:Cross-references: UNIPROT:P04049; GB:X03484; NID:g35841; PIDN:CAA27204.1; PID:g35842
R:Bonner, T.I.; Kerby, S.B.; Sutcliffe, P.; Gunnell, M.A.; Mark, G.; Rapp, U.R.
Mol. Cell. Biol. 5, 1400-1407, 1985
A:Title: Structure and biological activity of human homologs of the raf/ml oncogene.
A:Reference number: I57580; MUID:85295973; PMID:2993863
A:Accession: I57580
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 228-239, 'L', 241-541, 'I', 543-648 <BON2>
A:Cross-references: GB:L00212; NID:g190837; PIDN:AAA60247.1; PID:g496091
R:Morrison, D.K.; Heidicker, G.; Rapp, U.R.; Copeland, T.D.
J. Biol. Chem. 268, 17309-17316, 1993

A:Title: Identification of the major phosphorylation sites of the Raf-1 kinase.
A:Reference number: A43089; MUID:93352516; PMID:8349614
A:Contents: annotation; phosphorylation sites
A:Note: expression is ubiquitous in mammalian tissues that have been studied
C:Comment: After phosphorylation and activation by protein kinase C and other kinases,
C:Genetics:
A:Gene: GDB:RAF1
A:Cross-references: GDB:119546; OMIM:164760
A:Map position: 3p25-3p25
A:Introns: 278/3; 288/1; 330/3; 370/1; 398/2; 457/2; 473/1; 512/3; 556/3; 601/3
A:Note: the list of introns is incomplete
C:Function:
A:Description: catalyzes the formation of specific peptidyl-threonine-phosphate and pep
A:Pathway: MAP kinase cascade
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen
F:139-184/Domain: protein kinase C zinc-binding repeat homology <KZN>
F:347-613/Domain: protein kinase ATP-binding motif
F:355-363/Region: protein kinase ATP-binding motif
F:43.621/Binding site: phosphate (Ser) (covalent) #status experimental
F:139,165,168,184/Binding site: zinc (His, Cys, Cys) #status predicted
F:152,155,173,176/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:259/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experimental
F:268/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status experimental
F:375/Active site: Lys #status predicted
F:499/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 81.4%; Score 35; DB 1; Length 648;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
|||:||||
Db 377 LKVDPTP 384

RESULT 8
TVTRF6
Protein kinase raf-1 (EC 2.7.1.1) - rat
N:Alternate names: kinase-related transforming protein raf-1; raf-1 proto-oncogene prote
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: A26126
R:Ishikawa, F.; Takaku, F.; Nagao, M.; Sugimura, T.
Mol. Cell. Biol. 7, 1226-1232, 1987
A:Title: Rat c-raf oncogene activation by a rearrangement that produces a fused protein
A:Reference number: A26126; MUID:87172791; PMID:3550433
A:Accession: A26126
A:Molecule type: mRNA
A:Residues: 1-648 <ISH>
A:Cross-references: UNIPROT:P11345; GB:M15427; NID:g206544; PIDN:AAA42001.1; PID:g206545
C:Genetics:
A:Gene: raf
C:Function:
A:Description: signal transduction between cell membrane and nucleus; after phosphorylat
A:Pathway: MAP kinase cascade
A:Note: expression is ubiquitous in mammalian tissues that have been studied
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:139-184/Domain: protein kinase C zinc-binding repeat homology <KZN>
F:347-613/Region: protein kinase ATP-binding motif
F:43.621/Binding site: phosphate (Ser) (covalent) #status predicted
F:139,165,168,184/Binding site: zinc (His, Cys, Cys) #status predicted
F:152,155,173,176/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:259/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:268/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted
F:375/Active site: Lys #status predicted
F:499/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:499/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 81.4%; Score 35; DB 1; Length 648;
Best Local Similarity 75.0%; Pred. No. 36;

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Matches      6;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1  LKAMDPTP 8
      ||:||||
Db      377  LKVVDPTP 384

RESULT 9
G64225
ribosomal protein L21 homolog - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C:Accession: G64225
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.;
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: G64225
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-99 <TR>
A:Cross-references: UNIPROT:P47475; GB:U39701; GB:L43967; NID:g1045915; PID:g1045922; TI
A:Experimental source: strain G-37
C:Genetic code: SGC3
C:Superfamily: hypothetical protein yxB

Query Match      79.1%; Score 34; DB 2; Length 99;
Best Local Similarity 75.0%; Pred. No. 6.9;
Matches      6;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1  LKAMDPTP 8
      ||:||||
Db      60  LKLDPTP 67

RESULT 10
E87327
Hypothetical protein CC0632 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: E87327
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.;
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: E87327
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <STO>
A:Cross-references: UNIPROT:Q9AAAG8; GB:AE005673; NID:g13421843; PIDN:AAK22617.1; GSPDB:C
A:Genes: CC0632

Query Match      76.7%; Score 33; DB 2; Length 350;
Best Local Similarity 75.0%; Pred. No. 46;
Matches      6;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1  LKAMDPTP 8
      ||:||||
Db      15  LKALTPTP 22

RESULT 11
PD0001
protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13), liver - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C:Accession: PD0001

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R:Ikura, K.; Nasu, T.; Yokota, H.; Sasaki, R.; Chiba, H.
Agric. Biol. Chem. 51, 957-961, 1987
A:Title: Cloning of cDNA coding for guinea pig liver transglutaminase.
A:Reference number: PD0001
A:Accession: PD0001
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-444 <IKU>
A:Cross-references: UNIPROT:Q7M0F8
C:Superfamily: protein-glutamine gamma-glutamyltransferase
C:Keywords: aminoacyltransferase
F:89/Active site: Cys #status predicted

Query Match      76.7%; Score 33; DB 2; Length 444;
Best Local Similarity 62.5%; Pred. No. 61;
Matches      5;  Conservative      3;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1  LKAMDPTP 8
      ||:||||
Db      167  VQALDPTP 174

RESULT 12
TVXLRP
protein kinase raf-1 (EC 2.7.1.1) - African clawed frog
N:Alternate names: kinase-related transforming protein raf-1; raf-1 proto-oncogene prote
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: S01930; I51254
R:le Guellec, R.; le Guellec, K.; Paris, J.; Philippe, M.
Nucleic Acids Res. 16, 10357, 1988
A:Title: Nucleotide sequence of Xenopus C-raf coding region.
A:Reference number: S01930; MUID:89057471; PMID:3194203
A:Accession: S01930
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-638 <LEG>
A:Cross-references: UNIPROT:P09560; EMBL:X12948; NID:g65027; PIDN:CAA31407.1; PID:g65028
R:le Guellec, R.; Couturier, A.; Le Guellec, K.; Paris, J.; Le Fur, N.; Philippe, M.
Biol. Cell 72, 39-45, 1991
A:Title: Xenopus c-raf proto-oncogene: cloning and expression during oogenesis and early
A:Reference number: I51254; MUID:92096753; PMID:1721855
A:Accession: I51254
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-308, R', 310-638 <LEX>
A:Cross-references: GB:S74063; NID:g241259; PIDN:AAB20707.1; PID:g241260
C:Genetics:
A:Gene: raf
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: MAP kinase cascade
A>Note: after phosphorylation and activation by protein kinase C, phosphorylates and act
C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen
F:138-183/Domain: protein kinase C zinc-binding repeat homology <KZN>
F:338-604/Domain: protein kinase homology <KIN>
F:346-354/Region: protein kinase ATP-binding motif
F:43/Binding site: phosphate (Ser) (covalent) #status predicted
F:138,164,167,183/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:151,154,172,175/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:257/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:266/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predict
F:366,384,459,461/Active site: Lys, Glu, Asp, Lys #status predicted
F:490/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match      76.7%; Score 33; DB 1; Length 638;
Best Local Similarity 75.0%; Pred. No. 91;
Matches      6;  Conservative      0;  Mismatches      2;  Indels      0;  Gaps      0;

QY      1  LKAMDPTP 8
      ||:||||
Db      368  LKVTDPTP 375

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RESULT 13

A29996
protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A29996
R;Ikura, K.; Nasu, T.; Yokota, H.; Tsuchiya, Y.; Sasaki, R.; Chiba, H.
Biochemistry 27, 2898-2905, 1988
A;Title: Amino acid sequence of guinea pig liver transglutaminase from its cDNA sequence
A;Reference number: A29996; MUID:88294033; PMID:2900023
A;Accession: A29996
A;Molecule type: mRNA
A;Residues: 1-691 <IKU>
A;Cross-references: UNIPROT:P08587
A;Experimental source: liver
C;Superfamily: protein-glutamine gamma-glutamyltransferase
C;Keywords: aminocyltransferase
F;277/Active site: Cys #status predicted

Query Match 76.7%; Score 33; DB 1; Length 691;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
:::|||||
Db 355 VQALDPTP 362

RESULT 14

A34203
DNA-binding protein PRDII-BF1 - human
A;Alternate names: major histocompatibility complex enhancer-binding protein 1
C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34203; A34779
R;Fan, C.M.; Maniatis, T.
Genes Dev. 4, 29-42, 1990
A;Title: A DNA-binding protein containing two widely separated zinc finger motifs that
A;Reference number: A34203; MUID:90169514; PMID:2106471
A;Accession: A34203
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2717 <PAN>
A;Cross-references: UNIPROT:P15822; EMBL:X51435; NID:G38017; PIDN:CAA35798.1; PID:G38018
R;Baldwin Jr., A.S.; LeClair, K.P.; Singh, H.; Sharp, P.A.
Mol. Cell. Biol. 10, 1406-1414, 1990
A;Title: A large protein containing zinc finger domains binds to related sequence element
A;Reference number: A34779; MUID:90205817; PMID:2108316
A;Accession: A34779
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 801-1072, 'N', 1074-1168, 'K', 1170-1225, 'V', 1227-1434, 'N', 1436-1607, 'I', 1609-16
A;Cross-references: GB:M32019
C;Superfamily: HIV-EP2 enhancer-binding protein
C;Keywords: DNA binding; transcription regulation; zinc finger

Query Match 76.7%; Score 33; DB 2; Length 2717;
Best Local Similarity 85.7%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPTP 8
|||||
Db 579 KAMDPKP 585

RESULT 15

E64679
tryptophan synthase, alpha subunit - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: E64679

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: E64679
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-262 <TOM>
A;Cross-references: UNIPROT:P56141; GB:AE000632; GB:AE000511; NID:92314443; PIDN:AAD0832
C;Superfamily: tryptophan synthase alpha chain; tryptophan synthase alpha chain homology
F;17-244/Domain: tryptophan synthase alpha chain homology <TRPA>

Query Match 74.4%; Score 32; DB 2; Length 262;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
|||||
Db 198 LKAFSPTP 205

Search completed: May 26, 2005, 18:44:52
Job time : 14.64 secs

Page 1 of 1
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:18:07 ; Search time 61.12 Seconds
(without alignments)
67.026 Million cell updates/sec

Title: US-10-047-945-7
Perfect score: 43
Sequence: 1 LKAMDPTP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	17	Q9TR78	Q9tr78 didelphis m
2	43	100.0	140	Q8HZ75	Q8hz75 didelphis m
3	43	100.0	291	DM43_DIDMR	P82957 didelphis m
4	43	100.0	291	Q8HZ74	Q8hz74 didelphis m
5	38	88.4	274	Q95Q06	Q95qq6 caenorhabdi
6	35	81.4	301	Q19055	Q19055 papio hamad
7	35	81.4	308	Q9CU36	Q9cu36 mus musculu
8	35	81.4	314	Q8HYX5	Q8hyx5 didelphis m
9	35	81.4	323	1 RAP_MSV36	P00532 murine sarc
10	35	81.4	359	Q85453	Q85453 murine sarc
11	35	81.4	375	Q87624	Q87624 ic4 retrovi
12	35	81.4	380	1 MIL_AVIMH	P00531 avian retro
13	35	81.4	421	2 Q15278	Q15278 homo sapien
14	35	81.4	495	2 Q99N58	Q99n58 mus musculu
15	35	81.4	506	2 Q85632	Q85632 avian retro
16	35	81.4	647	1 RAF1_CHICK	P05625 gallus gall
17	35	81.4	648	1 RAF1_HUMAN	P04049 homo sapien
18	35	81.4	648	1 RAF1_MOUSE	Q99n57 mus musculu
19	35	81.4	648	1 RAF1_RAT	P11345 rattus norv
20	34	79.1	99	2 Y233_MYCE	P47475 mycoplasma
21	34	79.1	99	2 Q6CS74	Q6cs74 kluyveromyc
22	34	79.1	221	2 Q81725	Q81725 rupestris s
23	34	79.1	221	2 Q81902	Q81902 rupestris s
24	34	79.1	363	2 Q90Z88	Q90z88 xenopus lae
25	34	79.1	449	2 Q75817	Q75817 ashbya goss
26	34	79.1	534	2 Q7S1F7	Q7s1f7 neurospora
27	33	76.7	177	2 Q90WGO	Q90wgo seriola qui
28	33	76.7	182	2 Q87NP1	Q87npl vibrio para
29	33	76.7	189	2 Q43221	Q43221 triticum ae
30	33	76.7	194	2 Q9RJ27	Q9rj27 streptomyce
31	33	76.7	209	2 Q8P816	Q8p816 xanthomonas

32	33	76.7	209	2	Q8PJG8	Q8pjg8 xanthomonas
33	33	76.7	256	1	PCN2_PYRAB	Q8zy16 pyrobaculum
34	33	76.7	273	2	Q8LKF6	Q8lkf6 lycopersico
35	33	76.7	285	2	Q9DEB2	Q9deb2 seriola qui
36	33	76.7	297	2	Q8Y3G7	Q8y3g7 ralstonia s
37	33	76.7	342	2	Q9M3Z4	Q9m3z4 cicier ariet
38	33	76.7	350	2	Q9AAG8	Q9aag8 caulobacter
39	33	76.7	367	2	Q91T12	Q91tl2 heterobasid
40	33	76.7	368	2	Q7MU18	Q7mu18 porphyron
41	33	76.7	375	2	Q63C05	Q63c05 bacillus ce
42	33	76.7	375	2	Q6NH70	Q6nh70 corynebacte
43	33	76.7	375	2	Q813N0	Q813n0 bacillus ce
44	33	76.7	375	2	Q81JF3	Q81jf3 bacillus an
45	33	76.7	375	2	Q6HJF9	Q6hjf9 bacillus th

ALIGNMENTS

RESULT 1

Q9TR78	PRELIMINARY;	PRT;	17 AA.
AC	Q9TR78:		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)		
DE	ANTI-BOTHRUPIC complex 48,000 SUBUNIT (Fragment).		
OS	Didelphis marsupialis (Southern opossum).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.		
OX	NCBI_TaxID=9268;		
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=95149299; PubMed=7846694; DOI=10.1016/0041-0101(94)90353-0;		
RA	Perales J., Mousasche H., Marangoni S., Oliveira B., Domont G.B.;		
RT	"Isolation and partial characterization of an anti-bohrupic complex		
RT	from the serum of South American Didelphidae.";		
RL	Toxicon 32:1237-1249(1994).		
SQ	SEQUENCE 17 AA; 1947 MW; CB55FB40E73B2A2A CRC64;		

Query Match : 100.0%; Score 43; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
| | | | |
Db 1 LKAMDPTP 8

RESULT 2

Q8HZ75	PRELIMINARY;	PRT;	140 AA.
ID	Q8HZ75		
AC	Q8HZ75:		
DT	01-MAR-2003 (TrEMBLrel. 23, Created)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Alpha 1B glycoprotein DVOP51-D (Fragment).		
OS	Didelphis marsupialis virginiana (North American opossum).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.		
OX	NCBI_TaxID=9267;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Martinez M.E., Pierce J.R.;		
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY131000; AAN06911.1; -		
DR	HSSP; O76036; 10LL.		
DR	InterPro; IPR007110; Ig-like.		
FT	NON TER 1		
FT	NON TER 140		
SQ	SEQUENCE 140 AA; 15297 MW; E19D071A76AA5A7F CRC64;		

Query Match : 100.0%; Score 43; DB 2; Length 140;

Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
DB 42 LKAMDPTP 49

RESULT 3

ID DM43_DIDMR STANDARD; PRT; 291 AA.
AC P82857;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom metalloproteinase inhibitor DM43.
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]_SEQUENCE, AND MASS SPECTROMETRY.
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Serum;
RX MEDLINE=2193568; PubMed=11815628; DOI=10.1074/jbc.M200589200;
RA Neves-Ferreira A.G.C., Perales J., Fox J.W., Shannon J.D.,
RT Makino D.L., Garratt R.C., Domont G.B.;
RT "Structural and functional analyses of DM43, a snake venom
RT metalloproteinase inhibitor from Didelphis marsupialis serum.";
RL J. Biol. Chem. 277:13129-13137(2002).
CC -!- FUNCTION: Metalloproteinase inhibitor.
CC -!- SUBUNIT: Homodimer.
CC -!- TISSUE SPECIFICITY: Blood and milk.
CC -!- PTM: N-glycosylated.
CC -!- MASS SPECTROMETRY: MW=42691; METHOD=WALDI; RANGE=1-291;
CC -!- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR011015; LEM_like.
DR Pfam: PF00047; IG_1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Metalloprotease inhibitor; Repeat.
FT DOMAIN 22 79 IG-like V-type 1.
FT DOMAIN 114 171 IG-like V-type 2.
FT DOMAIN 191 288 IG-like V-type 3.
FT DISULFID 28 74 Potential.
FT DISULFID 121 163
FT DISULFID 213 265
FT CARBOHYD 23 23 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 156 156 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 160 160 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 175 175 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 291 AA; 32390 MW; 17A496227B69A65B CRC64;

Query Match 100.0%; Score 43; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
DB 1 LKAMDPTP 8

RESULT 4

ID Q8H274 PRELIMINARY; PRT; 291 AA.
AC Q8H274;
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha 1B glycoprotein DVOP114 (fragment).
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.

OX NCBI_TaxID=9267;
RN [1]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Martinez M.E., Pierce J.R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY131001; AAN06912.1; -.
DR HSP; Q8NHL6; IGX.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR Pfam: PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1_291
FT NON_TER 291
SQ SEQUENCE 291 AA; 32509 MW; BEC282838A1C0BF4 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
DB 1 LKAMDPTP 8

RESULT 5

ID Q95QO6 PRELIMINARY; PRT; 274 AA.
AC Q95QO6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein C55C3.6.
GN Name=C55C3.6; ORFNames=C55C3.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Woessne J., Stellyes L.;
RT "The sequence of C. elegans cosmid C55C3.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [5]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RN [6]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;

RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U53335; AAL27232.1; -.
 DR WormBase; WBGene00016956; C55C3.6.
 KW WormPep; C55C3.6; CE29736.
 KW Hypothetical protein.
 SQ SEQUENCE 274 AA; 30019 MW; D7EAE60465888DA4 CRC64;

Query Match 88.4%; Score 38; DB 2; Length 274;
 Best Local Similarity 87.5%; Pred. NO. 24;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
 |||||
 Db 133 LKPDPTP 140

RESULT 6

OL9055 PRELIMINARY; PRT; 301 AA.
 AC OL9055;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE C-RAF homolog (Fragment).
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OC NCBI_TaxID=9557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Maniyan S., Schumacher C., Gioffi C., Sharif H., Yuryev A., Lappe R.,
 RA Mondavi B., Hanson S., Goff S., Wennogle L.P.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AF006463; AAB63196.1; -.
 DR HSSP; P54763; 1UJA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot Kinase.
 DR InterPro; IPR008271; Ser Thr_kin_AS.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; PKinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON TER 1
 SQ SEQUENCE 301 AA; 34230 MW; 3512983ADF5D1A3B CRC64;

Query Match 81.4%; Score 35; DB 2; Length 301;
 Best Local Similarity 75.0%; Pred. NO. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
 |||||
 Db 30 LKVDPTP 37

RESULT 7

Q9CU36 PRELIMINARY; PRT; 308 AA.
 AC Q9CU36;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
 DE enriched library, clone:6430402F14 product:v-raf-1 leukemia viral
 DE oncogene 1, full insert sequence. (fragment).
 GN Name=Raf1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6875(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RA "High-efficiency full-length cDNA cloning";
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RA "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RA The FANTOM Consortium,
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RC Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horl F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AK018272; BAB31142.1; -.
 DR HSSP; P54763; 1UJA.
 DR MGD; MGI:97847; Raf1.
 DR GO; GO:0005829; C:cytosol; TAS.

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DR GO: GO:0005886; C:plasma membrane; TAS.
DR GO: GO:0005515; P:protein binding; IPI.
DR GO: GO:0004672; P:protein kinase activity; TAS.
DR GO: GO:0007243; P:protein kinase cascade; TAS.
DR InterPro; IPR011009; Kinase.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR08271; Ser Thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
SQ SEQUENCE 308 AA; 35058 MW; F87DDGABE27600BB CRC64;

Query Match 81.4%; Score 35; DB 2; Length 308;
Best Local Similarity 75.0%; Pred. NO. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
DB 37 LKVDPTP 44

RESULT 8
QHXYX PRELIMINARY; PRT; 314 AA.
AC Q8HYX5;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Venom metalloproteinase inhibitor DM43b precursor.
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Trugilho M.R.O., Junqueira-de-Azevedo I.L.M., Neves-Ferreira A.G.C.,
RA Domont G.B., Ho P.L., Perales J.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY163806; RAN64698.1; -.
DR HSSP; P24071; IOVZ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 314 venom metalloproteinase inhibitor DM43b.
SQ SEQUENCE 314 AA; 34604 MW; 69D55F54486D35A5 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 314;
Best Local Similarity 87.5%; Pred. NO. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
DB 24 LKAMDPTP 31

RESULT 9
RAF_MSV36 STANDARD; PRT; 323 AA.
AC P00532;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase transforming protein raf
DE (EC 2.7.1.37).

```

```

GN Name=V-RAF;
OS Murine sarcoma virus 3611.
OC Viruses; Retrovirdae; Retroviridae; Mammalian type C retroviruses.
OX NCBI_TaxID=11812;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84121298; PubMed=6320371;
RA Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
RT "A common onc gene sequence transduced by avian carcinoma virus MH2
RL and by murine sarcoma virus 3611.";
RN Science 223:813-816(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84172180; PubMed=6324342;
RA Mark G.E., Rapp U.R.;
RT "Primary structure of v-raf: relatedness to the src family of
RT oncogenes.";
RL Science 224:285-289(1984).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- MISCELLANEOUS: This protein is synthesized as a Gag-Raf
CC polyprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAF
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; K01691; AAA46579.1; ALT_INIT.
DR PIR; A00638; TVMVVF6.
DR HSSP; P54763; IJPA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot Kinase.
DR InterPro; IPR008271; Ser Thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Oncogene; Polyprotein; Serine/threonine-protein kinase;
KW Transferase.
FT DOMAIN 24 284 Protein kinase.
FT NP_BIND 30 38 ATP (By similarity).
FT BINDING 50 50 ATP (By similarity).
FT ACT_SITE 143 143 Proton acceptor (By similarity).
SQ SEQUENCE 323 AA; 36883 MW; 52A5423A66E362F3 CRC64;

Query Match 81.4%; Score 35; DB 1; Length 323;
Best Local Similarity 75.0%; Pred. NO. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
DB 52 LKVDPTP 59

RESULT 10
Q85453 PRELIMINARY; PRT; 359 AA.
AC Q85453;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE 3611 raf gene. (Fragment).
OS Murine sarcoma virus.
OC Viruses; Retrovirdae; Retroviridae; Mammalian type C retroviruses.
OX NCBI_TaxID=11802;
RN [1]
RP SEQUENCE FROM N.A.

```


RX MEDLINE=84121298; PubMed=6320371;
RA Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
RT "A common onc gene sequence transduced by avian carcinoma virus MH2
and by murine sarcoma virus 3611.";
RL Science 223:813-816(1984).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; X02084; AAA46576.1; -.
DR HSP; Q9WJP4; IEM4.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0019088; P:viral assembly; IEA.
DR InterPro; IPR003036; Gag_P30.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008916; Retro capsid C.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF02093; Gag_P30; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
SQ SEQUENCE 359 AA; 40935 MW; 5B6C615C5331570D CRC64;

Query Match 81.4%; Score 35; DB 2; Length 359;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
Db 88 LKVDPTP 95

RESULT 11
Q67624 PRELIMINARY; PRT; 375 AA.
AC Q67624
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE V-Mil protein.
GN Name=v-Mil;
OS IC4 retrovirus.
OC Viruses; Retrovirdae; Retroviridae.
OX NCBI_TaxID=36381;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94309138; PubMed=8035477;
RA Felder M.P., Laugier D., Yatsula B., Derzelee P., Calothy G., Marx M.;
RT "Functional and biological properties of an avian variant long
terminal repeat containing multiple A to G conversions in U3
sequence.";
RT J. Virol. 68:4759-4767(1994).
RL -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC EMBL; X77628; CAA54718.1; -.
DR HSP; P54763; IJPA.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR01245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 375 AA; 42459 MW; 7FB38E5C5B86DD09 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 375;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
Db 105 LKVDPTP 112

RESULT 12
MIL_AVMH STANDARD; PRT; 380 AA.
AC P00531;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serine/threonine-protein kinase transforming protein mil
(EC 2.7.1.37).
DE Name=v-Mil; Synonyms=v-MHT;
GN Avian retrovirus MH2.
OS Viruses; Retrovirdae; Retroviridae; Alpharetrovirus.
OC Viruses; Retrovirdae; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11870;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191511; PubMed=6325930;
RA Suttrave P., Bonner T.I., Rapp U.R., Jansen H.W., Patschinsky T.,
Bister K.;
RT "Nucleotide sequence of avian retroviral oncogene v-mil: homologue of
murine retroviral oncogene v-raf.";
RL Nature 309:85-88(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=6328485;
RA Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
RT "Nucleotide sequence of avian carcinoma virus MH2; two potential onc
genes, one related to avian virus MC29 and the other related to murine
sarcoma virus 3611.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3000-3004 (1984).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=84121298; PubMed=6320371;
RA Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
RT "A common onc gene sequence transduced by avian carcinoma virus MH2
and by murine sarcoma virus 3611.";
RL Science 223:813-816(1984).
CC -1- FUNCTION: By itself the v-Mil oncogene has only weak transforming
capacity but it abolishes the growth factor requirements of avian
macrophages transformed by other oncogenes.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- MISCELLANEOUS: This protein is synthesized as a Gag-Mht or Gag-Mil
polyprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAF
subfamily.
CC
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CC
CC EMBL; X00534; CAA25211.1; ALT_INIT.
DR PIR; A00639; TVFVMM.
DR HSP; P54763; IJPA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR Pfam; PF000069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Oncogene; Polyprotein; Serine/threonine-protein kinase;
KW Transferase.
FT DOMAIN 82 341 Protein kinase.
FT NP_BIND 88 96 ATP (By similarity).
FT BINDING 108 108 ATP (By similarity).
FT ACT_SITE 201 201 Proton acceptor (By similarity).
FT CONFLICT 211 211 G -> E (in Ref. 3).
SQ SEQUENCE 380 AA; 42853 MW; 6498695FB7EBE5D CRC64;

Query Match 81.4%; Score 35; DB 1; Length 380;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMPDTP 8
||:||||
DB 110 LKVDPTP 117

RESULT 13
Q15278 PRELIMINARY; PRT; 421 AA.
AC Q15278
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RAF1 protein (Fragment).
CN Name=RAF1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85295973; PubMed=2993863;
RA Bonner T.I., Kerby S.B., Sutcliffe P., Gunnell M.A., Mark G., Rapp U.R.;
RT "Structure and biological activity of human homologs of the raf/mil oncogene".
RL Mol. Cell. Biol. 5:1400-1407 (1985).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; L00212; AAA60247.1; JOINED.
DR EMBL; L00206; AAA60247.1; JOINED.
DR EMBL; L00208; AAA60247.1; JOINED.
DR EMBL; L00207; AAA60247.1; JOINED.
DR EMBL; L00209; AAA60247.1; JOINED.
DR EMBL; L00211; AAA60247.1; JOINED.
DR EMBL; M11376; AAA60247.1; JOINED.
DR EMBL; L00213; AAA60247.1; JOINED.
DR EMBL; L00210; AAA60247.1; JOINED.
DR PIR; S60341; S60341.
DR HSP; P06239; IQPC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 421 421
SQ SEQUENCE 421 AA; 47376 MW; F08DED75D91E8251 CRC64;

Query Match 81.4%; Score 35; DB 2; Length 421;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMPDTP 8
||:||||
DB 150 LKVDPTP 157

RESULT 14
Q99N58 PRELIMINARY; PRT; 495 AA.
AC Q99N58
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein kinase raf 1 (Fragment).
CN Name=RAF1; Synonyms=cRAF;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21481893; PubMed=11597136; DOI=10.1006/geno.2001.6627;
RA Gray T.A., Azama K., Whitmore K., Min A., Abe S., Nicholls R.D.;
RT "Phylogenetic conservation of the makorin-2 gene, encoding a multiple zinc-finger protein, antisense to the RAF1 proto-oncogene".
RL Genomics 77:119-126(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Doi M., Abe S.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB057655; BAB39748.1; --
DR HSP; F11345; IRRB.
DR MGD; MGI:97847; Raf1.
DR GO; GO:0005829; C:cytosol; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004672; F:protein kinase activity; TAS.
DR GO; GO:0007243; F:protein kinase cascade; TAS.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR003116; RBD.
DR Pfam; PF00130; Cl_1; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF02196; RBD; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; Cl_1; 1.
DR SMART; SM00455; RBD; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00898; RBD; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1 1
FT NON_TER 495 495
SQ SEQUENCE 495 AA; 55543 MW; B0AB53C2DAA287AE CRC64;

Query Match 81.4%; Score 35; DB 2; Length 495;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMPDTP 8

Db 367 LKVDPTP 374
|| :|||

RESULT 15

Q85632 Q85632 PRELIMINARY; PRT; 506 AA.
AC Q85632; Q85633;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gag protein (Fragment).
OS Avian retrovirus MH2.
OC Viruses; Retrovirdae; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11870;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84261423; PubMed=6086317;
RA Galibert F., de Dinechin S.D., Righi M., Stehelin D.;
RT "The second oncogene ml of avian retrovirus MH2 is related to the src
RT gene family.";
RL EMBO J. 3:1333-1338(1984).
DR EMBL; X00578; CAA25238.1; -.
DR HSP; O92954; 1D1D.
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0016032; P:viral life cycle; IEA.
DR InterPro; IPR000721; Gag_P24.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008916; Retrov_capsid_C.
DR Pfam; PF00607; Gag_P24; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Core protein; Polyprotein.
FT NON_TER 1
FT CHAIN 127 506 Potential.
SQ SEQUENCE 506 AA; 56266 MW; 0583CE415DC06F6C CRC64;

Query Match 81.4%; Score 35; DB 2; Length 506;
Best Local Similarity 75.0%; Pred. NO. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LKANDPTP 8
|| :|||
Db 236 LKVDPTP 243

Search completed: May 26, 2005, 18:43:27
Job time : 64.12 secs

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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:17:22 ; Search time 68.8 Seconds
(without alignments)
44.972 Million cell updates/sec

Title: US-10-047-945-7

Perfect score: 43

Sequence: 1 LKWDPTP 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	43	100.0	8	7 ABB80228	Abb80228 Synthetic
2	43	100.0	9	7 ABB80227	Abb80227 Synthetic
3	43	100.0	10	2 AAW53843	Aaw53843 N-terminu
4	43	100.0	10	7 ABB80222	Abb80222 Synthetic
5	43	100.0	11	7 ABB80226	Abb80226 Synthetic
6	43	100.0	12	7 ABB80225	Abb80225 Synthetic
7	43	100.0	15	2 AAW11575	Aaw11575 N-terminu
8	43	100.0	15	2 AAW53841	Aaw53841 N-terminu
9	43	100.0	15	7 ABB80223	Abb80223 Synthetic
10	35	81.4	29	1 AAP81131	Aap81131 C-raf-rel
11	35	81.4	94	4 AAO02179	Aao02179 Human pol
12	35	81.4	267	2 AAY43943	Aay43943 Yeast pro
13	35	81.4	344	7 ADF18626	Adf18626 Protein c
14	35	81.4	405	7 ABO62609	Abo62609 Klebsiell
15	35	81.4	615	6 ABU08102	Abu08102 Human kin
16	35	81.4	615	8 ABM82924	Abm82924 Human dia
17	35	81.4	648	2 AAR22560	Aar22560 Mouse mut
18	35	81.4	648	2 AAR22562	Aar22562 Mouse mut
19	35	81.4	648	2 AAR22563	Aar22563 Mouse mut
20	35	81.4	648	2 AAR25277	Aar25277 Human c-r
21	35	81.4	648	2 AAR22561	Aar22561 Mouse mut
22	35	81.4	648	2 AAR22559	Aar22559 Mouse c-r
23	35	81.4	648	2 AAR98215	Aar98215 Human Raf
24	35	81.4	648	2 AAW13107	Aaw13107 Human Raf
25	35	81.4	648	2 AAW17048	Aaw17048 Mutant mo

26	35	81.4	648	2 AAW17047	Aaw17047 Mutant mo
27	35	81.4	648	2 AAW17044	Aaw17044 Human c-r
28	35	81.4	648	2 AAW17045	Aaw17045 Mouse c-r
29	35	81.4	648	2 AAW17046	Aaw17046 Mutant mo
30	35	81.4	648	2 AAW17049	Aaw17049 Mutant mo
31	35	81.4	648	2 AAW62220	Aaw62220 Raf-1 pro
32	35	81.4	648	2 AAW95611	Aaw95611 Homo sapi
33	35	81.4	648	2 AAY08981	Aay08981 Human c-R
34	35	81.4	648	2 AAW30668	Aaw30668 Mutant mo
35	35	81.4	648	2 AAW30666	Aaw30666 Mutant mo
36	35	81.4	648	2 AAW30669	Aaw30669 Mutant mo
37	35	81.4	648	2 AAW30664	Aaw30664 Human c-r
38	35	81.4	648	2 AAW30667	Aaw30667 Mutant mo
39	35	81.4	648	2 AAW30665	Aaw30665 Mouse c-r
40	35	81.4	648	3 AAY94501	Aay94501 Human c-r
41	35	81.4	648	3 AAB42701	Aab42701 Human ORF
42	35	81.4	648	3 AAB08773	Aab08773 Amino aci
43	35	81.4	648	4 AAG67619	Aag67619 Amino aci
44	35	81.4	648	4 AAB70295	Aab70295 Human c-R
45	35	81.4	648	4 AAG67440	Aag67440 Amino aci

ALIGNMENTS

RESULT 1
ABB80228
ID ABB80228 standard; peptide; 8 AA.
XX
AC ABB80228;
XX
DT 06-NOV-2003 (first entry)
XX
DB Synthetic LTNF, LT-8.
XX
KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW saliva; ELISA.
XX
OS Synthetic.
XX
FN WO2003060471-A2.
XX
PD 24-JUL-2003.
XX
PF 14-JAN-2003; 2003WO-US001044.
XX
PR 14-JAN-2002; 2002US-00047945.
XX
PA (LIPP/) LIPPS B V.
XX
FA (LIPP/) LIPPS F W.
XX
PI Lipps BV, Lipps FW;
XX
XX WPI; 2003-636703/60.
XX
XX Assessing a human endogenous protein (e.g. IGE, nerve growth factor,
XX insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
XX asthma or diabetes, by employing an ELISA on a saliva sample from a
XX patient.
XX
XX Claim 7; Page 4; 24pp; English.
XX
XX The sequences given in ABB80222-28 represent lethal toxin neutralising
XX factor (LTNP) peptides which may be used for reducing elevated levels of
XX serum proteins selected from immunoglobulin E (IGE), nerve growth factor
XX (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
XX particular, the methods of the invention are useful for diagnosing and
XX treating conditions with elevated serum IGE levels, e.g. asthma,
XX diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid

CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 43; DB 7; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
 Db 1 LKAMDPTP 8
 |||||

RESULT 2
 ABB80227
 ID ABB80227 standard; peptide; 9 AA.
 XX
 AC ABB80227;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Synthetic LTNF, LT-9.
 XX
 KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.
 XX
 PN WO2003060471-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 14-JAN-2003; 2003WO-US001044.
 XX
 PR 14-JAN-2002; 2002US-00047945.
 XX
 PA (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.
 XX
 PI Lipps BV, Lipps FW;
 XX
 DR WPI; 2003-636703/60.
 XX
 PS Claim 7; Page 4; 24pp; English.
 XX
 CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 CC factor (LTNF) peptides which may be used for reducing elevated levels of
 CC serum proteins selected from immunoglobulin E (IGE), nerve growth factor
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 CC particular, the methods of the invention are useful for diagnosing and
 CC treating conditions with elevated serum IGE levels, e.g. asthma,
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of
 CC the protein may be monitored by assaying a human endogenous protein by

CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 CC sample using an anti-serum that is specific for the protein. Saliva
 CC collection is relatively non-invasive when compared to blood collection
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires
 CC clotting time before centrifugation to separate serum. Saliva proteins
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from
 CC serum requires a more complicated sandwich type ELISA

XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 43; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
 Db 1 LKAMDPTP 8
 |||||

RESULT 3
 AAW53843
 ID AAW53843 standard; peptide; 10 AA.
 XX
 AC AAW53843;
 XX
 DT 08-JUL-1998 (first entry)
 XX
 DE N-terminus of opossum LTNF.
 XX
 KW LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;
 KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
 KW histamine reaction treatment.
 XX
 OS Didelphis virginiana.
 XX
 PN US5744449-A.
 XX
 PD 28-APR-1998.
 XX
 PF 03-JUN-1996; 96US-00657163.
 XX
 PR 10-MAY-1993; 93US-00058387.
 PR 22-SEP-1994; 94US-00310340.
 XX
 PA (LIPP/) LIPPS B V.
 PA (LIPP/) LIPPS F W.
 XX
 PI Lipps FW, Lipps BV;
 XX
 DR WPI; 1998-271108/24.
 XX
 PT Lethal Toxin Neutralising Factor peptide from opossum - can neutralise
 PT venom(s) from all major families of poisonous snakes.
 XX
 PS Claim 7; Col 11; 11pp; English.
 XX
 CC This sequence represents the peptide of the invention. It is a Lethal
 CC Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic
 CC protein derived from an opossum. The peptide can be used in a method for
 CC treating a victim of envenomation from a poisonous snake, preferably a
 CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It
 CC is useful for the treatment of snake bites, sepsis, allergies caused by
 CC the environment and treatment of bee or scorpion stings or toxicities
 CC caused by plant or bacterial toxins. The peptide can also be used in
 CC histamine reaction treatment. The peptide can be used in envenomation
 CC treatment for a variety of snakes without prior identification of the
 CC snake. Being short it can be synthetically prepared rather than the
 CC current production in horses, where some people can show hypersensitivity
 CC to horse proteins
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 43; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKAMDPTP 8
 |||||
 DB 1 LKAMDPTP 8
 |||||

RESULT 4
 ABB80222
 ID ABB80222 standard; peptide; 10 AA.
 XX
 AC ABB80222;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Synthetic LTNP, LT-10.
 XX
 KW Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.
 XX
 FN WO2003060471-A2.
 XX
 PN 24-JUL-2003.
 XX
 PD 14-JAN-2003; 2003WO-US001044.
 XX
 PF 14-JAN-2002; 2002US-00047945.
 XX
 PR (LIPP/) LIPPS B V.
 XX (LIPP/) LIPPS F W.
 XX
 PA Lipps BV, Lipps FW;
 XX
 PI WPI; 2003-636703/60.
 XX
 DR Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
 XX insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 XX asthma or diabetes, by employing an ELISA on a saliva sample from a
 XX patient.
 XX
 PS Claim 7; Page 3; 24pp; English.
 XX
 CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 XX factor (LTNP) peptides which may be used for reducing elevated levels of
 XX serum proteins selected from immunoglobulin E (IgE), nerve growth factor
 XX (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 XX particular, the methods of the invention are useful for diagnosing and
 XX treating conditions with elevated serum IgE levels, e.g. asthma,
 XX diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 XX arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 XX Addison's disease or Hodgkin's disease) or depression. The efficacy of
 XX the protein may be monitored by assaying a human endogenous protein by
 XX performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 XX sample using an anti-serum that is specific for the protein. Saliva
 XX collection is relatively non-invasive when compared to blood collection
 XX for serum. Saliva can be centrifuged immediately, whereas blood requires
 XX clotting time before centrifugation to separate serum. Saliva proteins
 XX can be assayed by a simple ELISA test, whereas an assay of proteins from
 XX serum requires a more complicated sandwich type ELISA

Sequence 10 AA;
 Query Match 100.0%; Score 43; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKAMDPTP 8
 |||||
 DB 1 LKAMDPTP 8
 |||||

RESULT 5
 ABB80226
 ID ABB80226 standard; peptide; 11 AA.
 XX
 AC ABB80226;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Synthetic LTNP, LT-11.
 XX
 KW Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;
 KW saliva; ELISA.
 XX
 OS Synthetic.
 XX
 FN WO2003060471-A2.
 XX
 PN 24-JUL-2003.
 XX
 PD 14-JAN-2003; 2003WO-US001044.
 XX
 PF 14-JAN-2002; 2002US-00047945.
 XX
 PR (LIPP/) LIPPS B V.
 XX (LIPP/) LIPPS F W.
 XX
 PA Lipps BV, Lipps FW;
 XX
 PI WPI; 2003-636703/60.
 XX
 DR Assaying a human endogenous protein (e.g. IgE, nerve growth factor,
 XX insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
 XX asthma or diabetes, by employing an ELISA on a saliva sample from a
 XX patient.
 XX
 PS Claim 7; Page 4; 24pp; English.
 XX
 CC The sequences given in ABB80222-28 represent lethal toxin neutralising
 XX factor (LTNP) peptides which may be used for reducing elevated levels of
 XX serum proteins selected from immunoglobulin E (IgE), nerve growth factor
 XX (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
 XX particular, the methods of the invention are useful for diagnosing and
 XX treating conditions with elevated serum IgE levels, e.g. asthma,
 XX diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
 XX arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
 XX Addison's disease or Hodgkin's disease) or depression. The efficacy of
 XX the protein may be monitored by assaying a human endogenous protein by
 XX performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
 XX sample using an anti-serum that is specific for the protein. Saliva
 XX collection is relatively non-invasive when compared to blood collection
 XX for serum. Saliva can be centrifuged immediately, whereas blood requires
 XX clotting time before centrifugation to separate serum. Saliva proteins
 XX can be assayed by a simple ELISA test, whereas an assay of proteins from
 XX serum requires a more complicated sandwich type ELISA

Sequence 11 AA;
 Query Match 100.0%; Score 43; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKAMDPTP 8
 |||||

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Db      1 LKAMDPTP 8

RESULT 6
ABB80225
ID      ABB80225 standard; peptide; 12 AA.
XX
AC      ABB80225;
XX
XX      06-NOV-2003 (first entry)
DT
DE      Synthetic LTNP, LT-12.
XX
KW      Lethal toxin neutralising factor; LTNP; serum protein; immunoglobulin E;
KW      IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;
KW      ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;
KW      SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;
KW      Graves' disease; Addison's disease; Hodgkin's disease; depression;
KW      saliva; ELISA.
XX
OS      Synthetic.
XX
PN      WO2003060471-A2.
XX
PD
PP      24-JUL-2003.
XX
PR      14-JAN-2003; 2003WO-US001044.
XX
PA      (LIPP/) LIPPS B V.
PA      (LIPP/) LIPPS F W.
XX
PI      Lipps BV, Lipps FW;
XX
DR      WPI; 2003-636703/60.
XX
PT      Assaying a human endogenous protein (e.g. IGE, nerve growth factor,
PT      insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.
PT      asthma or diabetes, by employing an ELISA on a saliva sample from a
PT      patient.
XX
PS      Claim 7; Page 4; 24pp; English.
XX
CC      The sequences given in ABB80222-28 represent lethal toxin neutralising
CC      factor (LTNP) peptides which may be used for reducing elevated levels of
CC      serum proteins selected from immunoglobulin E (IGE), nerve growth factor
CC      (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In
CC      particular, the methods of the invention are useful for diagnosing and
CC      treating conditions with elevated serum IGE levels, e.g. asthma,
CC      diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
CC      arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,
CC      Addison's disease or Hodgkin's disease) or depression. The efficacy of
CC      the protein may be monitored by assaying a human endogenous protein by
CC      performing an enzyme-linked immunosorbent assay (ELISA) on a saliva
CC      sample using an anti-serum that is specific for the protein. Saliva
CC      collection is relatively non-invasive when compared to blood collection
CC      for serum. Saliva can be centrifuged immediately, whereas blood requires
CC      clotting time before centrifugation to separate serum. Saliva proteins
CC      can be assayed by a simple ELISA test, whereas an assay of proteins from
CC      serum requires a more complicated sandwich type ELISA
XX
SQ      Sequence 12 AA;

Query Match      100.0%; Score 43; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 LKAMDPTP 8
        |||||
Db      1 LKAMDPTP 8

RESULT 7
AAW11575
ID      AAW11575 standard; peptide; 15 AA.
XX
AC      AAW11575;
XX
XX      25-MAR-2003 (revised)
DT      20-MAR-1997 (first entry)
XX
DE      N-terminal peptide from lethal toxin neutralising factor.
XX
KW      Lethal toxin neutralising factor; LTNP; opossum; bee toxin;
KW      scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.
XX
OS      Didelphis virginiana.
XX
PN      US5576297-A.
XX
PD      19-NOV-1996.
XX
PP      22-SEP-1994; 94US-00310340.
XX
PR      10-MAY-1993; 93US-00058387.
XX
PA      (LIPP/) LIPPS B V.
PA      (LIPP/) LIPPS F W.
XX
PI      Lipps FW, Lipps BV;
XX
DR      WPI; 1997-011287/01.
XX
PT      Treatment of victims of bee or scorpion stings or plant or bacterial
PT      toxins - by admin. of lethal toxin-neutralising factor or its N-terminal
PT      peptide.
XX
PS      Claim 7; Col 9; 9pp; English.
XX
CC      The present sequence is from the N-terminus of a 68 kD protein purified
CC      from the serum of the opossum Didelphis virginiana. The full-length
CC      protein is a lethal toxin neutralising factor (LTNP). The use of purified
CC      LTNP or of the chemically synthesised 15mer N-terminal peptide for
CC      treating victims of bee stings, scorpion stings and bacterial or plant
CC      toxins is claimed. The patent disclosure does not provide any evidence
CC      for neutralising activity against these various toxins. There is evidence
CC      of significant neutralising activity of the opossum LTNP and the 15mer
CC      peptide against venom from snakes of the families Crotalidae, Elapidae,
CC      Hydroliidae and Viperidae. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ      Sequence 15 AA;

Query Match      100.0%; Score 43; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 LKAMDPTP 8
        |||||
Db      1 LKAMDPTP 8

RESULT 8
AAW53841
ID      AAW53841 standard; peptide; 15 AA.
XX
AC      AAW53841;
XX
XX      08-JUL-1998 (first entry)
DT
DE      N-terminus of opossum LTNP.
XX
KW      LTNP; lethal toxin neutralising factor; opossum; envenomation; therapy;
KW      anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;
KW      sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;
KW      histamine reaction treatment.

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RESULT 13
ADP18626
ID ADF18626 standard; protein; 344 AA.
XX
XX ADF18626;
AC
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Protein c-Raf-1 (aa305-648).
DE
XX
XX Human; c-Raf-1; oncoprotein E7; p21CIP1; cytostatic; gene therapy.
XX
XX Homo sapiens.
OS
XX
XX WO200308922-A2.
FN
XX
XX 30-OCT-2003.
PD
XX
XX 21-APR-2003; 2003WO-US012667.
PF
XX
XX 19-APR-2002; 2002US-0374245P.
PR
XX
XX (UVRP ) UNIV ROCHESTER.
PA
XX
XX Mccance D, Westbrook TF;
PI
XX
XX WPI; 2003-845498/78.
DR
XX
XX Identifying a compound that inhibits E7 cellular proliferation activity
PT by administering a compound to a system, where the system maintains Akt
PT activity and selecting a compound that decreases the amount of Akt.
PT
XX
XX Disclosure; SEQ ID NO 2; 119pp; English.
PS
XX
XX The present sequence is that of protein c-Raf-1 (amino acids 305-648).
CC
XX
XX Human papillomavirus oncoprotein E7 abrogates Raf-associated arrest and
CC prevents inhibition of cyclin E-CDK2 activity without disrupting Raf
CC induction of p21Cip1. E7 neither interacts with p21Cip1 nor derepresses
CC p21Cip1-associated CDK2 activity, but instead reduces the association
CC between p21Cip1 and cyclin E-CDK2 complexes. Raf down-regulates steady-
CC state levels of Akt, a regulator of p21Cip1 localisation, leading to loss
CC of p21Cip1 phosphorylation and accumulation of p21Cip1. E7 disrupts the
CC effects of Raf on Akt activity and prevents p21Cip1 nuclear accumulation.
CC Maintenance of Akt activity is necessary and sufficient to bypass Raf
CC arrest. The invention provides methods for identifying and using
CC inhibitors of E7 cell proliferation activity, and for identifying and
CC using compounds capable of promoting the nuclear localization of p21Cip1.
CC The methods can be used to inhibit aberrant cellular proliferation for
CC treatment of cancer.
XX
XX
XX Sequence 344 AA;
SQ
Query Match 81.4%; Score 35; DB 7; Length 344;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
Db 73 LKVDPTP 80
||:|||||
||:|||||

RESULT 14
ABO62609
ID ABO62609 standard; protein; 405 AA.
XX
XX ABO62609;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX Klebsiella pneumoniae polypeptide seqid 9126.
DE
XX
XX Recombinant expression vector; transcription regulatory element;
KW

```

```

KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
XX Klebsiella pneumoniae.
XX
XX US6610836-B1.
XX
XX 26-AUG-2003.
PD
XX
XX 27-JAN-2000; 2000US-00489039.
PF
XX
XX 29-JAN-1999; 99US-0117747P.
PR
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX
XX Breton GL, Osborne M;
XX
XX WPI; 2003-895346/82.
XX
XX N-PSDB; ACH96160.
DR
XX
XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
PT
XX
XX Disclosure; SEQ ID NO 9126; 932pp; English.
PS
XX
XX The invention describes a new isolated nucleic acid encoding a Klebsiella
CC pneumoniae polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against Klebsiella pneumoniae. This is the amino acid sequence of a
CC Klebsiella pneumoniae polypeptide of the invention
XX
XX
XX Sequence 405 AA;
SQ
Query Match 81.4%; Score 35; DB 7; Length 405;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
Db 186 IKARDPTP 193
||:|||||
||:|||||

RESULT 15
ABU08102
ID ABU08102 standard; protein; 615 AA.
XX
XX ABU08102;
AC
XX
XX 10-MAY-2003 (first entry)
DT
XX
XX Human kinase and phosphatase protein, KPP-3, INCYTE No.6464221CD1.
XX
XX Human; enzyme; kinase and phosphatase; KPP; cancer; cirrhosis;
XX cell proliferative disorder; arteriosclerosis; atherosclerosis;
XX hepatitis; paroxysmal nocturnal haemoglobinuria; polycythaemia vera;
XX psoriasis; primary thrombocytopaenia; developmental disorder;
XX renal tubular acidosis; anaemia; mental retardation; AIDS; epilepsy;
XX neurological disorder; Alzheimer's disease; Parkinson's disease;
XX autoimmune disorder; inflammatory disorder; allergy; asthma;
XX acquired immunodeficiency syndrome; autoimmune thyroiditis;
XX contact dermatitis; Crohn's disease; diabetes mellitus;
XX glomerulonephritis; Goodpasture's syndrome; gout; Graves' disease;
XX Hashimoto's thyroiditis; irritable bowel syndrome; multiple sclerosis;
XX osteoarthritis; osteoporosis; pancreatitis; Reiter's syndrome;
XX rheumatoid arthritis; Sjogren's syndrome; uveitis; infection.
XX
XX Homo sapiens.
OS
XX
XX WO2003012065-A2.
XX
XX 13-FEB-2003.
PD
XX
XX

```

Search completed: May 26, 2005, 18:36:58
Job time : 70.8 secs

PF 01-AUG-2002; 2002WO-US024521.
XX
PR 02-AUG-2001; 2001US-0309627P.
PR 07-AUG-2001; 2001US-0310933P.
PR 09-AUG-2001; 2001US-0311323P.
PR 07-SEP-2001; 2001US-0317820P.
PR 14-SEP-2001; 2001US-0322264P.
PR 28-SEP-2001; 2001US-0326098P.
PR 19-DEC-2001; 2001US-0343007P.
PR 15-MAR-2002; 2002US-0364494P.
PR 24-APR-2002; 2002US-0375539P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Baughn MR, Yue H, Wallia NK, He A, Au-Young JK, Lee SY;
PI Gietzen KJ, Lal PG, Elliott VS, Ison CH, Yang J, Lee EA, Li JK;
PI Emerling BM, Richardson TW, Warren BA, Hafalia AJA, Marquis JP;
XX
XX WPI; 2003-239519/23.
DR N-PSDB; ABX13149.
XX
XX New human kinases and phosphatases and polynucleotides, useful for
PT diagnosing, treating or preventing autoimmune or inflammatory disorders
PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
PT cancer or hepatitis.
XX
PS Claim 1; Page 159-160; 199pp; English.
XX
CC The invention relates to an isolated polypeptide, which is a human kinase
CC and phosphatase, KPP (KPP-1 to KPP-18). Also included are the encoding
CC polynucleotides KPP NA, recombinant polynucleotide comprising a promoter
CC sequence operably linked to KPP NA, a cell transformed with the
CC recombinant polynucleotide, a transgenic organism comprising the
CC recombinant polynucleotide; an anti-KPP antibody, screening for
CC ant/agonists of KPP, screening for compounds which bind to or alter the
CC activity or expression of KPP, microarray where at least one element is
CC KPP NA, generating an expression profile of a sample containing
CC polynucleotides and an array comprising different nucleotide molecules
CC affixed in distinct physical locations on a solid substrate (where at
CC least one of the nucleotide molecules comprises a first oligonucleotide
CC or polynucleotide sequence specifically hybridisable with at least 30
CC contiguous nucleotides of a target KPP NA). The kinases and phosphatases
CC (KPP) polypeptides, polynucleotides, agonists and antagonists are useful
CC for diagnosing, treating or preventing disorders associated with aberrant
CC expression of KPP, particularly cell proliferative disorders (e.g.
CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal
CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
CC thrombocytopaenia or cancer), developmental disorders (renal tubular
CC acidosis, anaemia or mental retardation), neurological disorders (e.g.
CC Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/
CC inflammatory disorders (e.g. AIDS, acquired immunodeficiency syndrome,
CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's
CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,
CC gout, Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,
CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
CC bacterial, fungal, parasitic, protozoan or helminthic infections. They
CC are also useful in the assessment of the effects of exogenous compounds
CC on the expression of nucleic acid and aa sequences of proteins associated
CC with KPP. The polynucleotides encoding KPP are useful for creating
CC transgenic animals to model human disease. The present sequence
XX represents a KPP protein of the invention
SQ Sequence 615 AA;

Query Match 81.4%; Score 35; DB 6; Length 615;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LKAMDPTP 8
|||:||||
DB 344 LKVDPTP 351

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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:43:39 ; Search time 52.48 Seconds
(without alignments)
52.587 Million cell updates/sec

Title: US-10-047-945-7

Perfect score: 43

Sequence: 1 LKAMDPTP 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	43	100.0	8	14	US-10-047-945-7
2	43	100.0	9	14	US-10-047-945-6
3	43	100.0	10	14	US-10-047-945-1
4	43	100.0	11	14	US-10-047-945-5
5	43	100.0	12	14	US-10-047-945-4
6	43	100.0	15	14	US-10-047-945-2
7	35	81.4	301	17	US-10-732-923-13683
8	35	81.4	323	17	US-10-732-923-13460
9	35	81.4	350	16	US-10-664-421-139
10	35	81.4	359	17	US-10-732-923-13459
11	35	81.4	375	17	US-10-732-923-13529
12	35	81.4	380	17	US-10-732-923-13465
13	35	81.4	410	17	US-10-732-923-13463

14	35	81.4	410	17	US-10-732-923-13464	Sequence 13464, A
15	35	81.4	410	17	US-10-732-923-13646	Sequence 13646, A
16	35	81.4	420	17	US-10-732-923-13648	Sequence 13648, A
17	35	81.4	506	17	US-10-732-923-13462	Sequence 13462, A
18	35	81.4	602	17	US-10-732-923-13440	Sequence 13440, A
19	35	81.4	647	17	US-10-732-923-13647	Sequence 13647, A
20	35	81.4	648	9	US-09-513-145-6	Sequence 6, Appli
21	35	81.4	648	14	US-10-060-065-17	Sequence 17, Appl
22	35	81.4	648	14	US-10-059-585-38	Sequence 38, Appl
23	35	81.4	648	14	US-10-440-341-3	Sequence 3, Appli
24	35	81.4	648	15	US-10-394-322A-55	Sequence 55, Appl
25	35	81.4	648	15	US-10-457-954-4	Sequence 4, Appli
26	35	81.4	648	16	US-10-408-765A-490	Sequence 490, App
27	35	81.4	648	17	US-10-926-543-90	Sequence 90, Appl
28	35	81.4	648	17	US-10-498-698-20	Sequence 20, Appl
29	35	81.4	648	17	US-10-732-923-13441	Sequence 13441, A
30	34	79.1	99	15	US-10-282-122A-63524	Sequence 63524, A
31	34	79.1	220	17	US-10-803-063-70	Sequence 70, Appl
32	34	79.1	221	17	US-10-803-063-5	Sequence 5, Appli
33	34	79.1	221	17	US-10-803-063-27	Sequence 27, Appl
34	34	79.1	537	16	US-10-437-963-194830	Sequence 194830,
35	34	79.1	1152	16	US-10-602-441-12	Sequence 12, Appl
36	33	76.7	57	15	US-10-424-599-284130	Sequence 284130,
37	33	76.7	80	15	US-10-424-599-253125	Sequence 253125,
38	33	76.7	179	15	US-10-424-599-151816	Sequence 151816,
39	33	76.7	285	17	US-10-732-923-13623	Sequence 13623, A
40	33	76.7	317	15	US-10-424-599-151815	Sequence 151815,
41	33	76.7	432	9	US-09-738-626-5192	Sequence 5192, Ap
42	33	76.7	432	17	US-10-494-675-6	Sequence 6, Appli
43	33	76.7	635	17	US-10-732-923-13622	Sequence 13622, A
44	33	76.7	638	17	US-10-732-923-13626	Sequence 13626, A
45	33	76.7	638	17	US-10-732-923-13627	Sequence 13627, A

ALIGNMENTS

RESULT 1

US-10-047-945-7
; Sequence 7, Application US/10047945
; Publication No. US2003015755A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BIRTE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (ISE) IMPLICATED DISORDERS
; FILE REFERENCE: FWPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
US-10-047-945-7

Query Match 100.0%; Score 43; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8

Db 1 LKAMDPTP 8

RESULT 2

US-10-047-945-6
; Sequence 6, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.
US-10-047-945-6

Query Match 100.0%; Score 43; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTP 8
DB 1 LKAMDPTP 8

RESULT 3
US-10-047-945-1
; Sequence 1, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-1

Query Match 100.0%; Score 43; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTP 8
DB 1 LKAMDPTP 8

RESULT 4
US-10-047-945-5
; Sequence 5, Application US/10047945

; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.
US-10-047-945-5

Query Match 100.0%; Score 43; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTP 8
DB 1 LKAMDPTP 8

RESULT 5
US-10-047-945-4
; Sequence 4, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.
US-10-047-945-4

Query Match 100.0%; Score 43; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.19; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKAMDPTP 8
DB 1 LKAMDPTP 8

RESULT 6
US-10-047-945-2
; Sequence 2, Application US/10047945
; Publication No. US20030157555A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, BINIE V.

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; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWLPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-2

Query Match      100.0%; Score 43; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
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Db 1 LKAMDPTP 8

RESULT 7
US-10-732-923-13683
; Sequence 13683, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13683
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-10-732-923-13683

Query Match      81.4%; Score 35; DB 17; Length 301;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
   |||
Db 30 LKVVDPTP 37

RESULT 8
US-10-732-923-13460
; Sequence 13460, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13460
; LENGTH: 323
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```
; TYPE: PRT
; ORGANISM: Murine sarcoma virus 3611
US-10-732-923-13460

Query Match      81.4%; Score 35; DB 17; Length 323;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
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Db 52 LKVVDPTP 59

RESULT 9
US-10-664-421-139
; Sequence 139, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 139
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-139

Query Match      81.4%; Score 35; DB 16; Length 350;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
   |||
Db 79 LKVVDPTP 86

RESULT 10
US-10-732-923-13459
; Sequence 13459, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13459
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Murine sarcoma virus
US-10-732-923-13459

Query Match      81.4%; Score 35; DB 17; Length 359;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
   |||
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Db      88 LKVDPTP 95

RESULT 11
US-10-732-923-13529
; Sequence 13529, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13529
; LENGTH: 375
; TYPE: PRT
; ORGANISM: IC4 retrovirus
US-10-732-923-13529

Query Match      81.4%; Score 35; DB 17; Length 375;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKAMDPTP 8
      ||:||||
Db      105 LKVDPTP 112

RESULT 12
US-10-732-923-13465
; Sequence 13465, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13465
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Avian myelocytomatosis virus MH2
US-10-732-923-13465

Query Match      81.4%; Score 35; DB 17; Length 380;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKAMDPTP 8
      ||:||||
Db      110 LKVDPTP 117

RESULT 13
US-10-732-923-13463
; Sequence 13463, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13463

Db      88 LKVDPTP 95

LENGTH: 410
TYPE: PRT
ORGANISM: Avian myelocytomatosis virus MH2
US-10-732-923-13463

Query Match      81.4%; Score 35; DB 17; Length 410;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKAMDPTP 8
      ||:||||
Db      140 LKVDPTP 147

RESULT 14
US-10-732-923-13464
; Sequence 13464, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13464
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Avian myelocytomatosis virus MH2
US-10-732-923-13464

Query Match      81.4%; Score 35; DB 17; Length 410;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKAMDPTP 8
      ||:||||
Db      140 LKVDPTP 147

RESULT 15
US-10-732-923-13646
; Sequence 13646, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13646
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-732-923-13646

Query Match      81.4%; Score 35; DB 17; Length 410;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKAMDPTP 8
      ||:||||
Db      140 LKVDPTP 147

Search completed: May 26, 2005, 19:18:09
Job time : 73.48 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 18:29:58 ; Search time 18.24 Seconds
(without alignments)
32.741 Million cell updates/sec

Title: US-10-047-945-7

Perfect score: 43

Sequence: 1 LKAMDPTP 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	10	1	US-08-657-163A-2
2	43	100.0	15	1	US-08-310-340A-1
3	43	100.0	15	1	US-08-657-163A-1
4	35	81.4	267	2	US-07-857-224B-42
5	35	81.4	315	1	US-08-571-758-12
6	35	81.4	315	1	US-08-909-984A-12
7	35	81.4	315	1	US-08-909-983-12
8	35	81.4	346	1	US-08-276-151-5
9	35	81.4	405	4	US-09-489-039A-9126
10	35	81.4	648	1	US-08-276-151-2
11	35	81.4	648	1	US-08-185-282-1
12	35	81.4	648	1	US-08-185-282-2
13	35	81.4	648	1	US-08-185-282-3
14	35	81.4	648	1	US-08-185-282-4
15	35	81.4	648	1	US-08-185-282-5
16	35	81.4	648	1	US-08-185-282-12
17	35	81.4	648	2	US-08-886-751A-6
18	35	81.4	648	3	US-09-209-668-13
19	35	81.4	648	3	US-08-971-207-1
20	35	81.4	648	4	US-08-207-954-3
21	34	79.1	220	3	US-09-574-141A-70
22	34	79.1	220	4	US-09-568-189A-70
23	34	79.1	221	3	US-09-081-320-5
24	34	79.1	221	3	US-09-081-320-27
25	34	79.1	221	3	US-09-574-141A-5
26	34	79.1	221	3	US-09-574-141A-27
27	34	79.1	221	3	US-09-707-780-5

28	34	79.1	221	3	US-09-707-780-27	Sequence 27, Appli
29	34	79.1	221	4	US-09-568-189A-5	Sequence 5, Appli
30	34	79.1	221	4	US-09-568-189A-27	Sequence 27, Appli
31	34	79.1	284	4	US-09-949-016-8093	Sequence 8093, Ap
32	33	76.7	432	4	US-09-602-777A-140	Sequence 140, App
33	33	76.7	471	4	US-09-902-540-13211	Sequence 13211, A
34	32	74.4	72	4	US-09-949-016-8760	Sequence 8760, Ap
35	32	74.4	117	4	US-09-134-000C-3881	Sequence 3881, Ap
36	32	74.4	274	4	US-09-543-681A-5055	Sequence 5055, Ap
37	32	74.4	399	4	US-09-543-681A-5325	Sequence 5325, Ap
38	32	74.4	512	3	US-09-356-818A-2	Sequence 2, Appli
39	32	74.4	548	1	US-08-247-902A-2	Sequence 2, Appli
40	32	74.4	548	5	PCT-US93-10541-2	Sequence 2, Appli
41	32	74.4	602	2	US-08-419-652-6	Sequence 6, Appli
42	32	74.4	685	5	PCT-US91-09784-4	Sequence 4, Appli
43	32	74.4	687	5	PCT-US91-09784-2	Sequence 2, Appli
44	32	74.4	705	4	US-09-949-016-10140	Sequence 10140, A
45	32	74.4	771	1	US-07-923-976-5	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-657-163A-2
; Sequence 2, Application US/08657163A
; Patent No. 574449
; GENERAL INFORMATION:
; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
; TITLE OF INVENTION: SYNTHETIC LIPIDS AND THEIR
; TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BINIE V. LIPPS
; STREET: 4509 MIMOSA DR.
; CITY: BELLAIRE
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
; SOFTWARE: MS WORD 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,163A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,340
; FILING DATE: 22 SEPTEMBER 1994
; CLASSIFICATION: 514
; APPLICATION NUMBER: 08/058,387
; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN R. CASPERSON
; REGISTRATION NUMBER: 28,198
; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-482-2961
; TELEFAX: 713-663-7290
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N

ORIGINAL SOURCE: SYNTHETIC
US-08-657-163A-2

Query Match 100.0%; Score 43; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
DB 1 LKAMDPTP 8

RESULT 2
US-08-310-340A-1
Sequence 1, Application US/08310340A
Patent No. 5576297

GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,340A
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/058, 387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELEPHONE: 713-723-6845
TELEFAX: 713-663-7290
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA; SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA
STRAIN: WILD
INDIVIDUAL ISOLATE: TEXAS WILD
DEVELOPMENTAL STAGE: ADULT
HAPLOTYPE:
TISSUE TYPE: BLOOD
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:
LIBRARY:
CLONE:
PUBLICATION INFORMATION:

AUTHORS: JONAS PERALES, ET AL.
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE
JOURNAL: INTERNATIONAL SOCIETY ON
JOURNAL: TOXINOLOGY
VOLUME: 10TH WORLD CONGRESS ON ANIMAL
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,
VOLUME: SINGAPORE
ISSUE: PROGRAMME AND ABSTRACTS
PAGES: 104
DATE: 3-8 NOV 1991
US-08-310-340A-1

Query Match 100.0%; Score 43; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
DB 1 LKAMDPTP 8

RESULT 3
US-08-657-163A-1
Sequence 1, Application US/08657163A
Patent No. 5744449

GENERAL INFORMATION:
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
TITLE OF INVENTION: SYNTHETIC LITNFS AND THEIR
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BINIE V. LIPPS
STREET: 4509 MIMOSA DR.
CITY: BELLAIRE
STATE: TEXAS
COUNTRY: USA
ZIP: 77401

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,163A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/310,340
FILING DATE: 22 SEPTEMBER 1994
CLASSIFICATION: 514
APPLICATION NUMBER: 08/058,387
FILING DATE: 10 MAY 1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
TELEPHONE: 713-482-2961
TELEFAX: 713-663-7290
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE: OPOSSUM SERA; SEQ ID NO: 1:
ORGANISM: DIDELPHIS VIRGINIANA

AUTHORS:

CC 3130A VHF F.R. 35

Qy 1 LKAMDPTP 8
||| : |||
pb 44 LKVPDPTP 51

RESULT 6
US-08-909-984A-12
; Sequence 12, Application US/08909984A
; Patent No. 5747275
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerry M.
; APPLICANT: Therrien, Marc
; APPLICANT: Chang, Henry C.
; APPLICANT: Karim, Felix D.
; APPLICANT: Wasarman, David A.
; TITLE OF INVENTION: A No. 5747275el Protein Kinase Required for Ras
; TITLE OF INVENTION: Signal Transduction
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,984A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B96-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-909-984A-12
; Query Match 81.4%; Score 35; DB 1; Length 315;
; Best Local Similarity 75.0%; Pred. No. 34;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LKAMDPTP 8
Db 44 LKVDPTP 51
RESULT 7
US-08-909-983-12
; Sequence 12, Application US/08909983
; Patent No. 5747288
; GENERAL INFORMATION:
; APPLICANT: Rubin, Gerry M.
; APPLICANT: Therrien, Marc
; APPLICANT: Chang, Henry C.
; APPLICANT: Karim, Felix D.
; APPLICANT: Wasarman, David A.
; TITLE OF INVENTION: A No. 5747288el Protein Kinase Required for Ras
; TITLE OF INVENTION: Signal Transduction
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,983
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/571,758
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B96-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-909-983-12
; Query Match 81.4%; Score 35; DB 1; Length 315;
; Best Local Similarity 75.0%; Pred. No. 34;
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LKAMDPTP 8
Db 44 LKVDPTP 51
RESULT 8
US-08-276-151-5
; Sequence 5, Application US/08276151
; Patent No. 5597719
; GENERAL INFORMATION:
; APPLICANT: Freed, Ellen
; APPLICANT: Ruggieri, Rosamaria
; TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward et al.
; STREET: Five Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,151
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Ph.D., Timothy E
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: ONYX-005/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5481
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids

; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE: C-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 US-08-276-151-5

Query Match 81.4%; Score 35; DB 1; Length 346;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
 || : ||||
 Db 75 LKVVDPTP 82

RESULT 9

US-09-489-039A-9126
 ; Sequence 9126, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 9126
 ; LENGTH: 405
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-9126

Query Match 81.4%; Score 35; DB 4; Length 405;
 Best Local Similarity 75.0%; Pred. No. 44;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
 || : ||||
 Db 186 IKARDPTP 193

RESULT 10

US-08-276-151-2
 ; Sequence 2, Application US/08276151
 ; Patent No. 5597719
 ; GENERAL INFORMATION:
 ; APPLICANT: Freed, Ellen
 ; APPLICANT: Ruggieri, Rosamaria
 ; TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Godward et al.
 ; STREET: Five Palo Alto Square
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/276.151
 ; FILING DATE: 14-JUL-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:

; NAME: Torchia, Ph.D., Timothy E
 ; REGISTRATION NUMBER: 36,700
 ; REFERENCE/DOCKET NUMBER: ONYX-005/000S
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 843-5481
 ; TELEFAX: (415) 857-0663
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 648 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-276-151-2

Query Match 81.4%; Score 35; DB 1; Length 648;
 Best Local Similarity 75.0%; Pred. No. 75;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
 || : ||||
 Db 377 LKVVDPTP 384

RESULT 11

US-08-185-282-1
 ; Sequence 1, Application US/08185282
 ; Patent No. 5618670
 ; GENERAL INFORMATION:
 ; APPLICANT: Rapp, Ulf R.
 ; APPLICANT: Storm, Stephen M.
 ; TITLE OF INVENTION: DETECTION METHOD FOR C-RAP-1 GENES
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
 ; STREET: 1615 L Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20036-5601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/185.282
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/759,738
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Scott, Watson T.
 ; REGISTRATION NUMBER: 26,581
 ; REFERENCE/DOCKET NUMBER: WTS/5683/82732
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 861-3000
 ; TELEFAX: (202) 822-0944
 ; TELEX: 6714627 CUSH
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 648 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-08-185-282-1

Query Match 81.4%; Score 35; DB 1; Length 648;
 Best Local Similarity 75.0%; Pred. No. 75;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8
 || : ||||
 Db 377 LKVVDPTP 384

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RESULT 12
US-08-185-282-2
; Sequence 2, Application US/08185282
; Patent No. 5618670
; GENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.
; APPLICANT: Storm, Stephen M.
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAP-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,282
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/82732
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-185-282-2
Query Match 81.4%; Score 35; DB 1; Length 648;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
Db 377 LKVDPTP 384

RESULT 13
US-08-185-282-3
; Sequence 3, Application US/08185282
; Patent No. 5618670
; GENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.
; APPLICANT: Storm, Stephen M.
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAP-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,282
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/82732
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-185-282-3
Query Match 81.4%; Score 35; DB 1; Length 648;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
Db 377 LKVDPTP 384
```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,282
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/82732
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-185-282-3
Query Match 81.4%; Score 35; DB 1; Length 648;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKAMDPTP 8
Db 377 LKVDPTP 384

RESULT 14
US-08-185-282-4
; Sequence 4, Application US/08185282
; Patent No. 5618670
; GENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.
; APPLICANT: Storm, Stephen M.
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAP-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,282
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/82732
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
US-08-185-282-4
Query Match      81.4%; Score 35; DB 1; Length 648;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LKAMDPTP 8
Db      377 LKVDPTP 384

RESULT 15
US-08-185-282-5
; Sequence 5, Application US/08185282
; Patent No. 5618670
; GENERAL INFORMATION:
; APPLICANT: Rapp, Ulf R.
; APPLICANT: Storm, Stephen M.
; TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,282
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,738
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/82732
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-185-282-5
Query Match      81.4%; Score 35; DB 1; Length 648;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LKAMDPTP 8
Db      377 LKVDPTP 384

Search completed: May 26, 2005, 19:08:41
Job time : 19.44 secs
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